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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:41:28 ; Search time 40 Seconds  
(without alignments)  
870.424 Million cell updates/sec

Title: US-09-940-919-2

Perfect score: 2750

Sequence: 1 MATLLRSKLSNVATSVNKS.....SGFVHSLGLEIAVRTNAED 525

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2700	98.2	525	US-09-178-093B-2	Sequence 2, Appli
2	858	31.2	486	US-09-178-093B-1	Sequence 1, Appli
3	429	15.6	149	US-09-270-767-31957	Sequence 31957, A
4	303	11.0	145	US-09-270-767-33686	Sequence 33686, A
5	303	11.0	145	US-09-270-767-48903	Sequence 48903, A
6	211.5	7.7	456	US-09-976-594-584	Sequence 584, App
7	209	7.6	412	US-09-311-021-42	Sequence 42, Appl
8	203.5	7.4	500	US-09-178-093B-26	Sequence 26, Appl
9	192.5	7.0	418	US-09-640-419C-25	Sequence 25, Appl
10	192	7.0	504	US-09-178-093B-28	Sequence 28, Appl
11	183.5	6.7	447	US-09-370-253-2	Sequence 2, Appli
12	181.5	6.6	504	US-09-919-497-67	Sequence 67, Appl
13	175	6.4	447	US-09-370-253-10	Sequence 10, Appl
14	174	6.3	452	US-09-640-419C-5	Sequence 5, Appli
15	173	6.3	446	US-09-640-419C-26	Sequence 6, Appli
16	164	6.0	447	US-09-370-253-6	Sequence 20813, A
17	156.5	5.7	399	US-09-248-796A-20813	Sequence 24, Appl
18	155.5	5.7	449	US-09-640-419C-24	Sequence 12, Appl
19	154	5.6	432	US-09-370-253-12	Sequence 27, Appl
20	153	5.6	462	US-09-640-419C-27	Sequence 20815, A
21	145.5	5.3	483	US-09-248-796A-20815	Sequence 20816, A
22	129.5	4.7	511	US-09-248-796A-20816	Sequence 2, Appli
23	128	4.7	485	US-08-362-512A-2	Sequence 4, Appli
24	128	4.7	485	US-08-964-939-2	Sequence 2, Appli
25	123.5	4.5	493	US-08-362-512A-4	Sequence 4, Appli
26	123.5	4.5	493	US-08-964-939-4	Sequence 5639, Ap
27	123	4.5	516	US-09-328-352-5639	

## ALIGNMENTS

### RESULT 1

US-09-178-093B-2  
; Sequence 2, Application US/09178093B

; Patent No. 6660846

; GENERAL INFORMATION:

; APPLICANT: Robert H. Edwards

; APPLICANT: Richard J. Reimer

; APPLICANT: Steve L. McIntire

; APPLICANT: Erik M. Jorgenson

; APPLICANT: Kim Schuske

; TITLE OF INVENTION: Vesicular Amino Acid Transported

; TITLE OF INVENTION: Composition and Method

; FILE REFERENCE: 2002-000530

; CURRENT APPLICATION NUMBER: US/09/178,093B

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/063,012

; PRIOR FILING DATE: 1997-10-23

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: CHAIN

; LOCATION: (1)..(525)

; OTHER INFORMATION: RUNC-47 polypeptide sequence

US-09-178-093B-2

Query Match 98.2%; Score 2700; DB 4; Length 525;

Best Local Similarity 98.5%; Pred. No. 4e-274;

Matches 518; Conservative 3; Mismatches 2; Gaps 2;

Qy	1	MATLLRSKLSNVATSVNKSQAQKSGMFMFQQAATDEAVGFAHCDLDFEHROGLQ	60
Db	1	MATLLRSKLSNVATSVNKSQAQKSGMFMFQQAATDEAVGFAHCDLDFEHROGLQ	60
Qy	61	DILKAEGPCGDEGAEPVEGDHYORGSGAPLPPSGSKDQ-VGGGEGFGHDKPKITAW	119
Db	61	DILKSEGEPCGDEGAEPVEGDHYORG-GAPLPPSGSKDQAVGAGGEGFGHDKPKITAW	119
Qy	120	EAGNVNTAIQGFVILGLPYAILHGGYLGFLIIIFAAVYCCYTGKILIACLYEENEDGEV	179
Db	120	EAGNVNTAIQGFVILGLPYAILHGGYLGFLIIIFAAVYCCYTGKILIACLYEENEDGEV	179
Qy	180	VRVDSYVALANACCAAPRPTLGGRVYVVAQIIELVMTCILYVYSGNLYMNSFPGLPVS	239
Db	180	VRVDSYVALANACCAAPRPTLGGRVYVVAQIIELVMTCILYVYSGNLYMNSFPGLPVS	239
Qy	240	QKSWSIATAVLLPCAFKLNKXAVSKFSLCTLAHFVINILVIAYCLSRDWAWEKVKF	299

Db 240 QKWSIIATAVLLPCLAKLKAYSKSLCTLAHFVINTLVIAVCLSRARDWAWEKVF 299  
 QY 300 YIDVKKPISIGIIVFSYTSQIFLPSLEGNNQSPSEHFCMMNTHAACVLLKGLFALVAY 359  
 Db 300 YIDVKKPISIGIIVFSYTSQIFLPSLEGNNQSPSEHFCMMNTHAACVLLKGLFALVAY 359  
 QY 360 LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPPFAAVEVLEKSLFQSGRAFFP 419  
 Db 360 LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPPFAAVEVLEKSLFQSGRAFFP 419  
 QY 420 ACYSGDGLKSWGLTLRCAIVFTLLMAIYVPHFALLMGLTSGTGAAGLCLFLLPSLFHLR 479  
 Db 420 ACYSGDGLKSWGLTLRCAIVFTLLMAIYVPHFALLMGLTSGTGAAGLCLFLLPSLFHLR 479  
 QY 480 LLWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525  
 Db 480 LLWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525

RESULT 2

US-09-178-093B-1  
 ; Sequence 1, Application US/09178093B  
 ; Patent No. 6660846  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert H. Edwards  
 ; APPLICANT: Richard J. Reimer  
 ; APPLICANT: Steve L. McIntire  
 ; APPLICANT: Erik M. Jorgenson  
 ; APPLICANT: Kim Schuske  
 ; TITLE OF INVENTION: Vesicular Amino Acid Transported  
 ; FILE REFERENCE: 2002-0005.30  
 ; CURRENT APPLICATION NUMBER: US/09/178,093B  
 ; CURRENT FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: 60/063,012  
 ; PRIOR FILING DATE: 1997-10-23  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 486  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1)...(486)  
 ; OTHER INFORMATION: UNC-47 polypeptide sequence  
 US-09-178-093B-1

Query Match 31.2%; Score 858; DB 4; Length 486;  
 Best Local Similarity 40.4%; Pred. No. 5.1e-81;  
 Matches 180; Conservative 96; Mismatches 141; Indels 28; Gaps 8;  
 QY 75 AEAPVEGDHYQSGAPLPSPGSKDQVGGGFGHDKPKITAEAGMNVTAIQMFV 134  
 Db 63 SEQPKODINQ-----EAKDD--GGE-----ASEPISALQANVTAIQMFI 107  
 QY 135 LGLPYAILHGGYGLFLIIPAAYVCCVTGKILIACTLYEENEDGVEVRDYSVAIANACC 194  
 Db 108 VGLPIAVKVGWWSIGAMVGVAVCYWTGVLLIECLYENG-----VKRKTYREIAD-FY 161  
 QY 195 APRPTLCGRVNVVAQIIELVMTCILYVVSGLMYSNFFCLPSYQSKSNSTIATVLLPC 254  
 Db 162 KPGF-----GKWLAAQITELLSTCIIIVLAADLQSCFFS--VDKAGWMNITSASLTC 215  
 QY 255 AFLKHLKAVSKFSLCTLAHFVINTLVIAVCLSRARDWAWEKVFYIDVKKPISIGIIV 314  
 Db 216 SFLDDLQIVSRSLSPFNALSHLVNLMVLYCLSPVQSWSPSTIFFSLNINTLPTIVGMV 275  
 QY 315 PSYTSQIFLPSLEGNNQSPSEHFCMMNTHAACVLLKGLFALVAILTWADETKVITDNL 374  
 Db 276 FGYSYTHFLNPLBGNMKNPAQFNVLKWSHTAAAVKVFVGMGLFTFGSLTQEEISNLS 335

QY 375 PG-STRAVNVIFLVAKALLSYPLPPFAAVEVLEKSLFQSGRAFFPACYSQDGLKSWGL 433  
 Db 336 PNOQSKILVNIILVKKALLSYPLPPFAAVQLLKNLFLGYPQTFTSCYSPDKSLREAV 395  
 QY 434 TURCALVVTLLMAIYVPHFALLMGLTSGTGAAGLCLFLLPSLFHLRLIMRKLWHQVFFD 493  
 Db 396 TURILVLFTLVALSVFVVELMGLVGNITGMLSFIPALPHLYIKEKTLNNEFRFD 455  
 QY 494 VAIFVIGICSVSGFVHSLGLEIEN 518  
 Db 456 QGIIMGCVICISGVYFSSMELRA 480

RESULT 3

US-09-270-767-31957  
 ; Sequence 31957, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 31957  
 ; LENGTH: 149  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-31957

Query Match 15.6%; Score 429; DB 4; Length 149;  
 Best Local Similarity 53.3%; Pred. No. 8.1e-37;  
 Matches 81; Conservative 27; Mismatches 40; Indels 4; Gaps 2;  
 QY 124 NVTNAIQGMFVGLPYAILHGGYGLFLIIPAAYVCCVTGKILIACTLYE-ENEDGEVVRV 182  
 Db 1 NVTNAIQGMFIVSLPFAVLHGGYWAIVAMVAGIAHICCVTKVLCVQCLYEPDPATGQWVRV 60  
 QY 183 RDSYVAIANACCAPRPTLGGRVNVNAQIIELVMTCILYVVSGLMYSNFFCLPSYQSKS 242  
 Db 61 RDSYVAIAKVCFGPK---LGAHVSIQIIELLMTCILYVVSGLDLAGTYPQGSFDSRS 117  
 QY 243 WSIITAVLLPCAFKLNKAVSKFSLCTLAH 274  
 Db 118 WMLFVGIFLLPMGLKSLKMWSTLSFWCTNGH 149

RESULT 4

US-09-270-767-33686  
 ; Sequence 33686, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 33686  
 ; LENGTH: 145  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-33686

Query Match 11.0%; Score 303; DB 4; Length 145;  
 Best Local Similarity 43.9%; Pred. No. 1.3e-23;  
 Matches 61; Conservative 26; Mismatches 52; Indels 0; Gaps 0;  
 QY 381 VVNIILVAKALLSYPLPPFAAVEVLEKSLFQSGRAFFPACYSQDGLKSWGLTLRCAV 440  
 Db 1 MYNFFLVKALLSYPLPYAACELLERNFFGPPKFTIWNLDGELKVLGFRVGI 60



160	IVVIYKFKQIPCIIVPELNSISANSTNADTCTPK---	YVTFNSKTYVALPTTAFVAFVCHP	216
322	FLPSSLEGNNQOQSFBEFCHNM--NWTTHAACVLKGLFALVAYLTWADETKEVITDNLPGS--	377	
217	SVLPIYSELKORSQKQMCMQMSNISFFAMFVYFLTALFGYLTFPDVMVQSDLLHHKYQSKDD	276	
378	-IRAVNIPLVAKALLSVPLPFFRAAVEVLEKSLFOEGSRAFFPACVSGDGRCLKSWGLTLIR	436	
277	ILILTVRLAVIAVILLTVPLVLF-----TVRSSUFELAKTKFNLCRH-----TVVT	323	
437	CALVVFETLLMAIYVPHFALMGLTSLTGAGLCFLPLPSLFHLRL-----WRKLIWHQV	490	
324	CILLVIVINLLVIFTPSMKDIIGVVGVTSANMLFILPSSLYLKITDQDGDKGTQRIWAAL	383	
491	PFDAIIVIGGICSVSGVFHSL	512	
384	FL-----GLGVLPSCQCHSL	397	

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RESULT 8
US-09-178-093B-26
; Sequence 26, Application US/09178093B
; Patent No. 6650846
; GENERAL INFORMATION:
; * APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgenson
; APPLICANT: Kim Schuske
; TITLE OF INVENTION: Vesicular Amino Acid Transported
; TITLE OF INVENTION: Composition and Method
; FILE REFERENCE: 2002-0005.30
; CURRENT APPLICATION NUMBER: US/09/178,093B
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063,012
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; - OTHER INFORMATION: synthetic peptide (RVT2) polypept
US-09-178-093B-26

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[illegible]

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350 LKGLFALVAYLTWADEKTEVITDNLPGS--IRAVNAIFLVAKALLSVPLPFAAEEVLEK 407
314 LVISLATIGYMCFRDEIKSGISITLNLPODMMLYOSVKILSGFIVTYSIQFYVPAEIIIP 373
408 SLFQSGRAFFPACYSGDGRILKSGGLTLRCLCALVFTLLMAIYVPHFALLMGLTSGLTGAG 467
374 AVTAELHAKWKICIDFG-----IRSLVSIITCAGAVLIPRLDIVISFVGAVSSST 423
468 LCFLLPSLPHURLLWRK---LLWHQVFFDVNAIFVIGGICSVSGFVHSLGSLIEAVETNA 523
424 LALILPPLVEI-LTFSKDHYNVW-MVLKNISIAFTGFVGLLGYTVVEIIL--YPTTA 478

RESULT 9
US-09-640-419C-25
; Sequence 25, Application US/09640419C
; Patent No. 6630615
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L
; APPLICANT: Crasta, Oswald R
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE
; FILE REFERENCE: 35718/193009 (5718-92)
; CURRENT APPLICATION NUMBER: US/09/640,419C
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,656
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/206,405
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-640-419C-25

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Query Match	7.0%;	Score 192.5;	DB 4;	Length 418;
Best Local Similarity	23.3%;	Pred. No. 2.5e-11;		
Matches	95;	Conservative 69;	Mismatches 169;	Indels 75; Gaps 16;
QY	114	PKITAEAGN-----NVTWAIQGMFLGLPYALLHGGV-LGLFLIFAAVCCVYTGKIL	166	
DB	19	PITAGRNNWYSYAFHNVT-AIVGAGVGLPYAWSELGNGPGVVVILLSWVILITFTQM	77	
QY	167	IACLVEENEDGEVVRDYSVAIENACCAPRFTPLGRVVNVAQIITELVMTCILYVYVSG	226	
DB	78	I-----EMHEMFEKGF-DRYHELQAAFGKK-----LGLYIWPQLLVETSACIVYMTVGG	129	
QY	227	-----NLMYNSPFGUVPVSOKSHSIITATVILPCAFLNKLVKAVSFSLICLTAHFVNI	279	
DB	130	ESLKIHOHLSVDGYECKRLKVRHPIILFASQFVLSLKNFNSISGSLVA--AVNYSVS	187	
QY	280	LVIAVCLSRAR-----DWAEKVKFVIDVKRKPISIGIIVFSYTS-----QIFLP	326	
DB	188	STIAWVASLTGVANNVEYGYKRNNTSVPLAFGLGEMAFAYAGHNVVLSIQATIPST	247	
QY	327	-EGNNQOQSPSEFCMMWTHIAACVLKGLFALVAYLTWADETKEVITDNL--PGSTR	383	
DB	248	PENPSKRPWKGAIVAYIIAFCYFP--VALVGFWTFGNVNESINIKTLRGPGLII	305	
QY	384	ITLVAKALLS--YLPPEFAAVEVLEKSLFQEGSRAPFFPACYGSDGRLLKSW-----	432	
DB	306	IVTIHLMGYSQVAMPVDFMIESV-----MIKWNHFSPTVRLR	344	
QY	433	LTALRCALVVFTLLMAIYVHPHALMGLTGLTGAGLCFLPLPSLFHURL	480	
DB	345	FTIRTFVAAATMGVALVHPHSALLSPFGGFIAPTYTFIPCIWIIL	392	

## RESULT 10

```

US-09-178-093B-28
; Sequence 28, Application US/09178093B
; Patent No. 8660846
; GENERAL INFORMATION:
; APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgensen
; APPLICANT: Kim Schuske
; TITLE OF INVENTION: Vesicular Amino Acid Transported
; FILE REFERENCE: 2002-0005.30
; CURRENT APPLICATION NUMBER: US/09/178,093B
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063,012
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (RVT3 polypeptide sequence)
US-09-178-093B-28

Query Match 7.0%; Score 192; DB 4; Length 504;
Best Local Similarity 20.3%; Pred. No. 3.7e-11;
Matches 102; Conservative 96; Mismatches 166; Indels 138; Gaps 24;

QY 57 GLQMDILKAEBCPCD-----EGEAPVEGDHYQEGSCAPLPPSGKQDQVGGGEGFGHD 112
DB 16 GKLEGLLPVGMPTADTORAEDQ-----HCEGKGKF-LQQSSKE----- 55
QY 113 KPKITAME-----AGNNVTNAIQGMFVLGPYAILHGG-YLGLFLIIFAAVVCCYTGK 164
DB 56 -PHTDFGKTSFGMSVENLSAINGSGILGLAYAMANTGIILFLTLTAVALLSSYSIH 114
QY 165 ILIACLYBENDEGEVVRVDSYVAIANACAPRPTLGRVNVVAQIIELV--MTCILYV 222
DB 115 LLL-----KSSGIVGIR-AYEQIGYRA-----FQTPGKLAALAILQNGAMSSYLI 162
QY 223 VVSG-NLAVNFPFGLPVSKSM-----SIITAVLLPCAFKLNKAV----- 263
DB 163 IKSELPLVIQTLNLEKTFPVWMDGNVLVLSVIIILPLALMRQLGYSYSGFSLSC 222
QY 264 -----SKFSLTLTAHFVIN-----ILVI-----AYCLSRADW 292
DB 223 MYFFLIAVIYKFKQVPCPLAHLNLTGNFHMVVEKSQLQSEBPDFAEACTP----- 277
QY 293 AWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNWQBPSEPHCMNNWTHIAACVLKG 352
DB 278 -----SYFTLNSQTAYTIPIMAFVCHPEVLPVTELDKPSK-RKMOHINSLSIAYVYV 331
QY 353 LF---ALVAYLTWADETKEVIDNL-----PGSIRAV-VNIFLVAKALLSYPLPFAAVEV 404
DB 332 MYFLAALPGYLFYDGVSELLHTYSKVDPPDVLILCVRAVLIAVTLTVPLPVRRA 391
QY 405 LEKSLPQEGSRAPFPACYSQDGLKSWGLTLRCALVWFTL-----LMAIYVPHFALLMGL 459
DB 392 IQQMLFQ--NQEF-----SW-----LRHVLIATGLTLCINLLVIFAPNLIGIFGI 434
QY 460 TGSLTGAGLCFLPLSLFHLRL 481
DB 435 IGATSAAPCLIFIPFAIFYFRIM 456

RESULT 11
US-09-370-253-2
; Sequence 2, Application US/09370253
; Patent No. 6165792
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.

```

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; APPLICANT: Sakai, Hajime
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Amino Acid Transporters
; FILE REFERENCE: BB-1200
; CURRENT APPLICATION NUMBER: US/09/370,253
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 60/097,222
; EARLIER FILING DATE: August 20, 1998
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-370-253-2

Query Match 6.7%; Score 183.5; DB 3; Length 447;
Best Local Similarity 22.1%; Pred. No. 2.4e-10;
Matches 96; Conservative 80; Mismatches 197; Indels 61; Gaps 15;

QY 119 WEAGNVTNAIQGMFVLGPYAILHGGY-LGLFLIIFAAVVCCYTGKILIACLYBENEDG 177
DB 39 WYSAPHNVTAMVGAGVLSLPYAMSELGMPGIAVMTLSWIIIVYT-----LWQVVENH 91
QY 178 EYVRVR--DSYVAIANACAPRPTLGRVNVVAQIIELVMTCILYVVVSGNLMYNSPFG 235
DB 92 EMVPGKRPDRYHELGOHAFGDK--LGLWIVVPQQLVVEVSLNIVMTGTGNSL-KKFHD 147
QY 236 LPVSQKSMI-----IATAVLLPCAFKLNKAYKPSLLCTLAHFVNILVIAVCLSR 288
DB 148 VICDGRCKDKLTFTIMIFASVHFLVLSQLPNFNSIGISLAAAVMSLSYSTAWGASLHK 207
QY 289 ARDAWEKVKFYI-----DVKKPISIGIIVFSYTS-----QIFLPSLEGN-MQOP 333
DB 208 GKE---ENDYSLRASTTAGQVFGGLGGLDVAFSYSGHNVLVLEIQATIPSTPGNPSKP 264
QY 334 SEPHCMNNWTHIAACVLKGLFALVAYLTWADETKE--VTIDNLPGSIRAVNIFLVAKAL 391
DB 265 MWKGVVVAVITIIAACYFP--VAFIGYAFGNSYDDNLTILNKPWLIIAAMNMMVVVHLI 322
QY 392 LSPFLPFAAVEVLEKSLFQEGSRAPFPACYSQDGLKSWGLTL-----RCALVVFLLMA 447
DB 323 GSYQIVAMPVDFMMETFLVKK--LEFAP-----GITRLRITTIYVAFMTFIG 368
QY 448 IYVPHFALLMGLTSGTLTGAGLCFLPLSLFHLRLMKLLWQHVFVDAIVFVIGGICSVSG 507
DB 369 MSFPFGGLIGFPGGLAFAPTTFYFLPCIMWLLICKRIFSLSWFTNWCIVLGLVLLMIVA 428
QY 508 FVHSLGLELIEAYRT 521
DB 429 PIGGLRQIIISAKT 442

RESULT 12
US-09-919-497-67
; Sequence 67, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-67

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Db	79	ITLVT-----LWQVMVEMHVPCKRFDRIYHELGQHAFGDK--LGLWIVVPPQQLIVE 128
Qy	216	MTCILYVVYSGNLMYNSPPGLPVSSQKSWSI-----IATAVLLPCAFLNKNLKA VSKFSL 268
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Db	188	AAA-----VMSLSYSIT-----AWGASVDKGN-VDDYDNLRAVTTCKVGFPGFAG 234
Qy	312	IIVFSVTS-----QIFLPSL-EGNQQPSEPCMNWTHIAACVLKGLFALVAVLTWA 363
Db	235	EVAFAGACHNVVLEIQATIPSTPEKPSKKPMKGVVAYIVVACYFP--VALIGYWAFG 292
Qy	364	DETKE--VITDNLPGSIAVNI FLVAKALLS---YPLPFFAAVE-VLEKSI.FQEGSRAP 417
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Qy	418	FPACTSGDGRLKSWGLTI-----RCALVYFTLLMAIYVPHFALLMGLTSGLTAGLCFLLP 473
Db	346	FPP-----GLTLRLIARTLYAFTMFVAITFPFPGGLGFGFGFAFAPTYFLP 394
Qy	474	SUFHLRLWRK--LLMHQVFFDVAIFVIGIC 503
Db	395	CINWLAIVKPFKFSLSW-----FTNWGCVILGVC 423

RESULT 14  
US-09-640-419C-5  
; Sequence 5, Application US/09640419C  
; Patent No. 6630615  
; GENERAL INFORMATION:  
; APPLICANT: Bidnev, Dennis I.

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; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE
;
; FILE REFERENCE: 35718/199009 (5718-92)
;
; CURRENT APPLICATION NUMBER: US/09/640,419C
;
; CURRENT FILING DATE: 2000-08-17
;
; PRIOR APPLICATION NUMBER: 60/149,656
;
; PRIOR FILING DATE: 1999-08-18
;
; PRIOR APPLICATION NUMBER: 60/206,405
;
; PRIOR FILING DATE: 2000-05-23
;
; NUMBER OF SEQ ID NOS: 28
;
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 5
;
; LENGTH: 452
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; TYPE: PRT
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; ORGANISM: Helianthus annuus
;
; US-09-640-419C-5

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Best Local Similarity	22.9%;	Pred. No. 2.4e-09;		
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QY	178	EVVRVR--DSYVAIANACCAPRPTTIGGRVNVVAQIIBLVMTCLIVVYVSGNLMYNSFPG	235	
Db	96	EMVPGKPRDYHBLGHOAFGEK--LGLYIVVPOQLVVEVSLCIYVMVTGGKSL-QKPHD	151	
QY	236	LPVSQKS-----WSIATAVLLPCAPLKNLKAVSFSLCLTIAHFVINILVIAYCLS	287	
Db	152	LLVRQDEQDIRLTFPIIMIVGSHVFLSHLPNFNSLGSGLAAIMSLSYSTIANGASLD	211	
QY	288	RA-----RDWAEKVKYIDVKKFPISIGIIIVFSYTS-----QIFPLSL-EGNMQOPSE	335	
Db	212	KGQPNVEYGYKAKSTTGTTFNPLGALGDMAFAYAGHNVLVEIQATIPSTPEKPSKGFMM	271	
QY	336	PHCMNMWTHIAACVLKGLFALVAYLTWADETKE--VITDNLPGSGIRAVNIFLVAKALLS	393	

RESULT 13  
; PRIOR APPLICATION NUMBER: 60/149,656

RESULT 13  
 US-09-370-253-10  
 ; PRIOR FILING DATE: 1999-08-18  
 ; PRIOR APPLICATION NUMBER: 60/206,405  
 ; Sequence 10, Application US/09370253

REQUEST FOR APPLICATION US/035/0233  
 ;  
 PATENT NO. 6165792  
 ;  
 PRIOR FILING DATE: 2000-05-23  
 ;  
 NUMBER OF SEQUENCES  
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000000  
GENERAL INFORMATION:  
NUMBER OF SEQ ID NOS: 8  
SCHEMATIC DIAGRAM VIEW  
SOFTWARE

APPLICANT: Allen, Stephen M.  
SOFTWARE: PatentIn Ver. 2.1  
SEO ID NO 5

APPLICANT: Sakai, Hajime

; APPLICANT: Thorpe, Catherine J.  
; ;  
; LENGTH: 432  
; TYPE: PRT

TITLE OF INVENTION: Amino Acid Transporters

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DEED. FILE NO.:  
ORGANISM: Helianthus annuus

; CACRATION: HELIANTHUS ANNUUS  
 US-09-640-419C-S  
 FILE REFERENCE: BB-1200  
 CREATING 2 MAR 24 1960  
 CREATING 2 MAR 24 1960

: CURRENT APPLICATION NUMBER: US/09/370,253  
ATTORNEY REF NO. 100000000

[illegible]

Best Local Similarity 22.9%; Pred. No. 2.4e-09;  
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Matches	100;	Conservative	70;	Mismatches	201;	Indels	66;	Gaps	17;
EARLIER FILING DATE:	August 20, 1998								
NUMBER OF SEQ ID NOS.	18								

NUMBER OF  
SEQ ID NOS: 18  
SOFTWARE: Microsoft Office 97

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; SOFTWARE: MICROSOFT OFFICE 97
; SOFIWARE: MICROSOFT OFFICE 97
; SEQ ID NO 10
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; TYPE: PRT

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US-09-370-253-10

DB 96 EMVPGKRRFDYHELGQHAFEK---LGLYTVVPOOIWVESLCITYMTGGKSI--CKEHD 151

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QY 236 LPVSKS-----WSIATVLLPCAFKLNKAVSKFSLLCTIAHFVINITVIAVCL 287

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112 DRPKITAW-----EAGW-----NVTNAIQGMFVLGIPYAILHGQY-LGLFLIIFAAV 157

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QY 158 VCCVTGKILIIACIYEENEDGEVVR--DSVVAIANACCAREPTVCCRVVVAQITRLV 215  
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Db 428 PIGGLRTI 435  
Search completed: November 8, 2004, 18:56:47  
Job time : 48 secs

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QY 505 VSGFVHSLGLEIAYRT 521  
Db 431 VVAPIGGLRSIIVQAKT 447

RESULT 15  
US-09-640-419C-26  
; Sequence 26, Application US/09640419C  
; Patent No. 6630615  
; GENERAL INFORMATION:  
; APPLICANT: Bidney, Dennis L  
; APPLICANT: Crasta, Oswald R  
; APPLICANT: Hu, Xu  
; APPLICANT: Lu, Guihua  
; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE  
; FILE REFERENCE: 35718/19009 (5718-92)  
; CURRENT APPLICATION NUMBER: US/09/640/419C  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,656  
; PRIOR FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: 60/206,405  
; PRIOR FILING DATE: 2000-05-23  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-640-419C-26

Query Match 6.3%; Score 173; DB 4; Length 446;  
Best Local Similarity 23.1%; Pred No. 3e-09;  
Matches 99; Conservative 71; Mismatches 186; Indels 72; Gaps 19;  
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QY 178 EVVVR--DSYVAIANACCAPRPTLGGRVNVVAQIIELVMTCILYVVVSGNLMVNSPFG 235  
Db 92 EMVPGKFRDRYHELQHAERK---LGLYIVVPOQLIVEIGVICIVVMTGKSL-KKEHE 147  
QY 236 L-----PVSQKSWSIATAVLLPCAFKLNKAVS-KFSLCTLAHFVN-----ILVIAY 284  
Db 148 LVCDDCKPIKLTIVFIMFASVHFLSHLPNENSISGSCCRRYVSQLNNRMGIISKOR 207  
QY 285 CLSRARDNAWEKVFIDVKKPISIGIIVPSYTS-----OILPSL-EGNMQQPSEF 336  
Db 208 C-SRRRSIRLOSNNRYYVNFPSGLGDVAFAYAGHNVVLEIQATIPPEKPSKGPWR 266  
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QY 394 --YPLPFFAAVEVL--EKSIFQSGRAFPACYSGBGRKSKNGLTUCALVVTLLMAIY 449  
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QY 450 VPHFALLMGLTGSITGAGLCFLPLSLFHLRL--WRKLLMHQVDFDVAIFV-- 498  
Db 370 FPFPGGLAFPGGFAFAPTYFLPCVWLAIYKPKYSLSWAN--WVCIVFGLFLMVL 427

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:44:35 ; Search time 173 Seconds  
(without alignments)  
1071.928 Million cell updates/sec

Title: US-09-940-919-2

Perfect score: 2750  
Sequence: 1 MATLLRSKLSNVATSVSNKS.....SGFVHSLEGLIEAYRTNAED 525

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 35325886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2750	100.0	525	9	US-09-871-503-2
2	2750	100.0	525	9	US-09-940-919-2
3	2750	100.0	525	11	US-09-972-211-34
4	2750	100.0	525	11	US-09-972-211-105
5	2750	100.0	525	14	US-10-239-566-2
6	2750	100.0	525	15	US-10-096-625-34
7	2750	100.0	525	15	US-10-096-625-105
8	2750	100.0	525	16	US-10-789-241-10
9	2746	99.9	525	11	US-09-972-211-30
10	2746	99.9	525	11	US-09-972-211-38
11	2746	99.9	525	15	US-10-096-625-30
12	2746	99.9	525	15	US-10-096-625-38
13	2742	99.7	525	11	US-09-972-211-36

14	2742	99.7	525	15	US-10-096-625-36	Sequence 36, Appl
15	2739	99.6	525	11	US-09-972-211-32	Sequence 32, Appl
16	2739	99.6	525	11	US-09-972-211-40	Sequence 40, Appl
17	2739	99.6	525	15	US-10-096-625-32	Sequence 32, Appl
18	2739	99.6	525	15	US-10-096-625-40	Sequence 40, Appl
19	2731	99.3	525	11	US-09-972-211-103	Sequence 103, App
20	2731	99.3	525	15	US-10-096-625-103	Sequence 103, App
21	2700	98.2	525	11	US-09-972-211-104	Sequence 104, App
22	2700	98.2	525	15	US-10-096-625-104	Sequence 104, App
23	2700	98.2	1050	14	US-10-225-810-36	Sequence 36, Appl
24	2641	96.0	521	11	US-09-972-211-106	Sequence 106, App
25	2641	96.0	521	15	US-10-096-625-106	Sequence 106, App
26	1075	39.1	549	11	US-09-972-211-107	Sequence 107, App
27	1075	39.1	549	15	US-10-096-625-107	Sequence 107, App
28	858	31.2	462	14	US-10-369-493-5867	Sequence 5867, Ap
29	858	31.2	486	14	US-10-225-810-37	Sequence 37, Appl
30	375	13.7	577	15	US-10-425-114-65034	Sequence 65034, A
31	372.5	13.5	496	17	US-10-425-115-301852	Sequence 301852, A
32	368	13.4	578	15	US-10-425-114-65416	Sequence 65416, A
33	364	13.2	555	17	US-10-425-115-357602	Sequence 357602, A
34	357.5	13.0	531	17	US-10-739-930-9570	Sequence 9570, Ap
35	355	12.9	496	16	US-10-437-963-201705	Sequence 201705, A
36	352.5	12.8	550	15	US-10-424-599-182680	Sequence 182680, A
37	352	12.7	522	17	US-10-425-115-216062	Sequence 216062, A
38	348.5	12.7	548	16	US-10-437-963-156455	Sequence 156455, A
39	343	12.5	430	15	US-10-425-114-58549	Sequence 58549, A
40	335	12.2	706	16	US-10-437-963-145638	Sequence 145638, A
41	324	11.8	370	15	US-10-080-334-136	Sequence 136, App
42	324	11.8	370	15	US-10-080-334-142	Sequence 142, App
43	323.5	11.8	438	17	US-10-425-115-297771	Sequence 297771, A
44	323.5	11.8	475	17	US-10-425-115-297768	Sequence 297768, A
45	323.5	11.8	487	15	US-10-425-114-68137	Sequence 68137, A

## ALIGNMENTS

## RESULT 1

US-09-871-503-2  
; Sequence 2, Application US/09871503  
; Patent No. US20020076758A1  
; GENERAL INFORMATION:  
; APPLICANT: George Christian Terstappen  
; APPLICANT: Cinzia Felicitia Sala  
; TITLE OF INVENTION: POLYPEPTIDE  
; FILE REFERENCE: QS 1013  
; CURRENT APPLICATION NUMBER: US/09/871,503  
; PRIOR APPLICATION NUMBER: 2001-05-31  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 525  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-871-503-2

Query Match	100.0%;	Score 2750;	DB 9;	Length 525;
Best Local Similarity	100.0%;	Pred. No. 2.1e-253;		
Matches 525;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MATLLRSKLSNVATSVSNKSQAKMGFMFGFQAATDEEAVGFAHCDLDFEHRLQGM 60		
Db	1	MATLLRSKLSNVATSVSNKSQAKMGFMFGFQAATDEEAVGFAHCDLDFEHRLQGM 60		
Qy	61	DILKAEGECGDEGAPVEGDHIVQSGCAPLPSSGKDQVGGGEGFGHDKPKITAVE 120		
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 Db 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFFAAVEVLEKSLFQEGSRAPFPA 420  
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 Db 421 CYSGDGRKLSWGLTLRCALVVTLLMAIYVPHFALLMGLTGLTGAGLCFLPLSLFHLRL 480  
 QY 481 LWRKLLHQVDFDVAIFVIGGICSVSGFVHSLGLELIEAYRTNAED 525  
 Db 481 LWRKLLHQVDFDVAIFVIGGICSVSGFVHSLGLELIEAYRTNAED 525

RESULT 2  
 ; Sequence 2, Application US/09940919  
 ; Patent No. US20020082390A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Friddle, Carl Johan  
 ; APPLICANT: Gerhardt, Brenda  
 ; APPLICANT: Hu, Yi  
 ; TITLE OF INVENTION: Same  
 ; FILE REFERENCE: Same  
 ; CURRENT APPLICATION NUMBER: US/09/940,919  
 ; CURRENT FILING DATE: 2001-08-28  
 ; PRIOR APPLICATION NUMBER: US 60/230,178  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-940-919-2

Query Match 100.0%; Score 2750; DB 9; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-253;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFFAAVEVLEKSLFQEGSRAPFPA 420  
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 Db 421 CYSGDGRKLSWGLTLRCALVVTLLMAIYVPHFALLMGLTGLTGAGLCFLPLSLFHLRL 480  
 QY 481 LWRKLLHQVDFDVAIFVIGGICSVSGFVHSLGLELIEAYRTNAED 525  
 Db 481 LWRKLLHQVDFDVAIFVIGGICSVSGFVHSLGLELIEAYRTNAED 525

RESULT 3  
 US-09-972-211-34  
 ; Sequence 34, Application US/09972211  
 ; Publication No. US20040048245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shimkets, Richard A  
 ; APPLICANT: Taupier Jr, Raymond J  
 ; APPLICANT: Burgess, Catherine E  
 ; APPLICANT: Zerhusen, Bryan D  
 ; APPLICANT: Mezes, Peter S  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Malyankar, Uriel M  
 ; APPLICANT: Grosse, William M  
 ; APPLICANT: Alsobrook II, John P  
 ; APPLICANT: Lepley, Denise M  
 ; APPLICANT: Spytek, Kimberly Ann  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: MacDougall, John R  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Stone, David J  
 ; APPLICANT: Smithson, Glennda  
 ; APPLICANT: Szekeres Jr, Edward S  
 ; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th  
 ; FILE REFERENCE: 21402-141  
 ; CURRENT APPLICATION NUMBER: US/09/972,211  
 ; PRIOR FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,325  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,323  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,400  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,397  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,401  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,379  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,402  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 30/238,384  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,373  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,372  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,383  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,382  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/275,892

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; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-34

Query Match          100.0%; Score 2750; DB 11; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.1e-253;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVSNKSKQKSGMPFARMGFOAATDEEAVGFACDDDLDFEHRQGLQM 60
DB 1 MATLLRSKLSNVATSVSNKSKQKSGMPFARMGFOAATDEEAVGFACDDDLDFEHRQGLQM 60
QY 61 DILKAEGPCDGEAEAPVEGDIIHYQSGGAPLPSPGSKDQVGGGEGFGHDKPKITAW 120
DB 61 DILKAEGPCDGEAEAPVEGDIIHYQSGGAPLPSPGSKDQVGGGEGFGHDKPKITAW 120
QY 121 AGWNVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIACLYEENEDGEV 180
DB 121 AGWNVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIACLYEENEDGEV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSPPGLPV 240
DB 181 RVRDSYVAIANACCAPRPTLGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSPPGLPV 240
QY 241 KWSIIATAVLLPCAFLNKLVKSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAFLNKLVKSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNWNTHIAACVLKGLFALVAY 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNWNTHIAACVLKGLFALVAY 360
QY 421 CYSGDGLKSWGLTIRCALVFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLFHLRL 480
DB 421 CYSGDGLKSWGLTIRCALVFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLFHLRL 480
QY 481 LWRKLLHQVFFDVAIFVIGICSVSGFVHSLGLELIEAYRTNAED 525
DB 481 LWRKLLHQVFFDVAIFVIGICSVSGFVHSLGLELIEAYRTNAED 525
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## RESULT 4

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US-09-972-211-105
; Sequence 105, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkerts, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R

Query Match          100.0%; Score 2750; DB 11; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.1e-253;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVSNKSKQKSGMPFARMGFOAATDEEAVGFACDDDLDFEHRQGLQM 60
DB 1 MATLLRSKLSNVATSVSNKSKQKSGMPFARMGFOAATDEEAVGFACDDDLDFEHRQGLQM 60
QY 61 DILKAEGPCDGEAEAPVEGDIIHYQSGGAPLPSPGSKDQVGGGEGFGHDKPKITAW 120
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QY 121 AGWNVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIACLYEENEDGEV 180
DB 121 AGWNVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIACLYEENEDGEV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSPPGLPV 240
DB 181 RVRDSYVAIANACCAPRPTLGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSPPGLPV 240
QY 241 KWSIIATAVLLPCAFLNKLVKSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAFLNKLVKSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNWNTHIAACVLKGLFALVAY 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNWNTHIAACVLKGLFALVAY 360
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us-09-940-919-2.rapb

Fri Nov 12 12:23:21 2004

RESULT 6  
US-10-096-625-34  
; Sequence 34, Application US/10096625  
; Publication No. US20040068095A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zernusen, Bryan D  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Spytek, Kimberly Ann  
; APPLICANT: Li, Li  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John R  
; APPLICANT: Gunther, Erik  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David J  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Szekeres Jr, Edward S  
; APPLICANT: Ji, Weizhen  
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th  
; TITLE OF INVENTION: Methods Of Using The Same  
; FILE REFERENCE: 21402-141 CIP  
; CURRENT APPLICATION NUMBER: US/10/096,625  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: 09/972,211  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/238,325  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,323  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,400  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,397  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,401  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,379  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,402  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 30/238,384  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,373  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,372  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,383  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,382  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/275,892  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/296,860  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 525  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-096-625-34

Query Match 100.0%; Score 2750; DB 15; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e-253;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-096-625-34

US-10-239-566-2  
; Sequence 2, Application US/10239566  
; Publication No. US20030089398A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; TITLE OF INVENTION: New human GABA recetor  
; FILE REFERENCE: VGATFRWS  
; CURRENT APPLICATION NUMBER: US/10/239,566  
; CURRENT FILING DATE: 2002-09-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 525  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-566-2

Query Match 100.0%; Score 2750; DB 14; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e-253;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-239-566-2

QY 1 MATLRSLKSNVATSVNKSQAKNSGMFARMGFOATDEAVGFACDLDLDFEHRGLOM 60  
DB 1 MATLRSLKSNVATSVNKSQAKNSGMFARMGFOATDEAVGFACDLDLDFEHRGLOM 60  
QY 61 DILKAEGEPCDEGAEPVEGDHYQSGAPLPPSGSKDQVGGGEGFGHDXPKITAME 120  
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QY 121 AGNVTNAIQGMFVLGYPAILHGGYLGFLIFPAAVVCCVTGKILIACLYEENDEGVV 180  
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DB 181 RVRDSYVAIANACCAPRPTLGGRVNVAQIIELVMTCILYVVVSGNMTNSPGLPVSQ 240  
QY 241 KWSIIATAVLLPCAFILKLVKAVSKFSLCTLAHFVNILVIAVCLSRADWAEVKFY 300  
DB 241 KWSIIATAVLLPCAFILKLVKAVSKFSLCTLAHFVNILVIAVCLSRADWAEVKFY 300  
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFFHCMMNTHIAACVLKGLFALVAYL 360  
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFFHCMMNTHIAACVLKGLFALVAYL 360  
QY 361 TWADETKEVITDNLPGSRVAVNIPLVAKALLSYPLPFAAIVEVLEKSLFOEGSRAFFPA 420  
DB 361 TWADETKEVITDNLPGSRVAVNIPLVAKALLSYPLPFAAIVEVLEKSLFOEGSRAFFPA 420  
QY 421 CYSGDGRKLSWGLTLRCALVVFLLMAIYVPHFALLMGLTSLTGAGLCFLPLSLPHRL 480  
DB 421 CYSGDGRKLSWGLTLRCALVVFLLMAIYVPHFALLMGLTSLTGAGLCFLPLSLPHRL 480  
QY 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525  
DB 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525

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QY 1 MATLLRSKLSNVATSVSNKQKMGFMFARMGFOAATDEEAVGFAHCDDLDLFEHROGLQW 60
Db 1 MATLLRSKLSNVATSVSNKQKMGFMFARMGFOAATDEEAVGFAHCDDLDLFEHROGLQW 60
QY 61 DILKAEPCGDEGAEAPVEGDHYQKSGAPLPPSGSKDQVGGGEGFGHDKPKITAVE 120
Db 61 DILKAEPCGDEGAEAPVEGDHYQKSGAPLPPSGSKDQVGGGEGFGHDKPKITAVE 120
QY 121 AGWNVNNAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIAACLYEENEDGEV 180
Db 121 AGWNVNNAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIAACLYEENEDGEV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRVNVAQIIELVMTCTILYVYVSGNLMYNSPPGLPVSQ 240
Db 181 RVRDSYVAIANACCAPRPTLGGRVNVAQIIELVMTCTILYVYVSGNLMYNSPPGLPVSQ 240
QY 241 KWSIIATATVLLPCAPLKNLKAWSKSLCTLAHFVNITLIVIAVCLSRARDWAEKVKFY 300
Db 241 KWSIIATATVLLPCAPLKNLKAWSKSLCTLAHFVNITLIVIAVCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNMTHTIAACVLKGLFALVAYL 360
Db 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNMTHTIAACVLKGLFALVAYL 360
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Db 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPPFAAVEVLEKSLFOEGSRAFFPA 420
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RESULT 7

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US-10-096-625-105
; Sequence 105, Application US/10096625
; Publication No. US20040068095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Mazes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glenda
; APPLICANT: Szekeres Jr, Edward S
; APPLICANT: Ji, Weizhen
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th
; FILE REFERENCE: 21402-141 CIP
; CURRENT APPLICATION NUMBER: US/10/096,625
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325

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; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-096-625-105

Query Match      100.0%; Score 2750; DB 15; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.le-253;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVSNKQKMGFMFARMGFOAATDEEAVGFAHCDDLDLFEHROGLQW 60
Db 1 MATLLRSKLSNVATSVSNKQKMGFMFARMGFOAATDEEAVGFAHCDDLDLFEHROGLQW 60
QY 61 DILKAEPCGDEGAEAPVEGDHYQKSGAPLPPSGSKDQVGGGEGFGHDKPKITAVE 120
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QY 121 AGWNVNNAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIAACLYEENEDGEV 180
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QY 241 KWSIIATATVLLPCAPLKNLKAWSKSLCTLAHFVNITLIVIAVCLSRARDWAEKVKFY 300
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QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNMTHTIAACVLKGLFALVAYL 360
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QY 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPPFAAVEVLEKSLFOEGSRAFFPA 420
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QY 421 CYSGDGRKLSWGLTLRCLVAVFTLLMAIYVPHFALLMGLTGTAGLCLFLLPSLPHRL 480
Db 421 CYSGDGRKLSWGLTLRCLVAVFTLLMAIYVPHFALLMGLTGTAGLCLFLLPSLPHRL 480
QY 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525

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Db 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525
; Sequence 10, Application US/10789241
; Publication No. US20040180332A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5860, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MPI03-041PIRNONNIM
; CURRENT APPLICATION NUMBER: US/10789,241
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/454,202
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/456,326
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/465,240
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/475,233
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/478,952
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/487,836
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/500,111
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Fas-SEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-10

Query Match 100.0%; Score 2750; DB 16; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.1e-253;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATLLRSKLSNVATSVNSKQAKXGWFARMGFQAATDEAVGFACDDLDLFEHROGLQ 60
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Qy 61 DILKAEGEPCDGEAEPVEGDHYQRGSGAPLPSPGSKDQVGGGEGFGHDKPKITAVE 120
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Qy 241 KWSIIATAVLLPCAFILKNIKAYSKESLLCTIAHFVNILIVIAVCLSRARDNAWEKV 300
Db 241 KWSIIATAVLLPCAFILKNIKAYSKESLLCTIAHFVNILIVIAVCLSRARDNAWEKV 300
Qy 301 IDVKKFPISIGIVFVSYSQIFLPSLEGNNQQPSEFHCMMNTHIAACVLKGLFALVAYL 360
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Qy 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLKSLFOEGSRAPFPA 420
Db 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLKSLFOEGSRAPFPA 420
Qy 421 CYSGDGRKLSWGLTLRCLAVVFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLPHRL 480
Db 421 CYSGDGRKLSWGLTLRCLAVVFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLPHRL 480

RESULT 8
US-10-789-241-10
; Sequence 10, Application US/10789241
; Publication No. US20040180332A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5860, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MPI03-041PIRNONNIM
; CURRENT APPLICATION NUMBER: US/10789,241
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/454,202
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/456,326
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/465,240
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/475,233
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/478,952
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/487,836
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/500,111
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Fas-SEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-10

Db 421 CYSGDGRKLSWGLTLRCLAVVFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLPHRL 480
Qy 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525
Db 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525

RESULT 9
US-09-972-211-30
; Sequence 30, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Maryankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-30
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Query Match      99.9%; Score 2746; DB 11; Length 525;
Best Local Similarity 99.8%; Pred. No. 5.1e-253;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVSNKSQAQKMGFMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQ 60
DB 1 MATLLRSKLSNVATSVSNKSQAQKMGFMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQ 60
QY 61 DILKAEPCGDEGAEPVEGDHYQRGSGAPLPSSGKQVGGGEGFGHDKPKITAW 120
DB 61 DILKAEPCGDEGAEPVEGDHYQRGSGAPLPSSGKQVGGGEGFGHDKPKITAW 120
QY 121 AGNVTNAIQGMFVLGFLPYAILHGGYGLFLIIFAAVVCCYTGKILIACLYEENEDGEV 180
DB 121 AGNVTNAIQGMFVLGFLPYAILHGGYGLFLIIFAAVVCCYTGKILIACLYEENEDGEV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRRVNVVAQIIELVMTCILYVVSNGMLMNSFFGLPV 240
DB 181 RVRDSYVAIANACCAPRPTLGGRRVNVVAQIIELVMTCILYVVSNGMLMNSFFGLPV 240
QY 241 KWSIIATAVLLPCAFKXNLKAVSKFSLICTLAHFVINILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAFKXNLKAVSKFSLICTLAHFVINILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTHTIAACVLKGLFALVAY 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTHTIAACVLKGLFALVAY 360
QY 361 TWADETKEVITDNLPGSIRAVVNIPLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFPA 420
DB 361 TWADETKEVITDNLPGSIRAVVNIPLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFPA 420
QY 421 CYSGDGRKLSWGLTLRUCALVFTLLMALIYVPHFALLMGLTGLSLGAGLCFLPLSLFHLRL 480
DB 421 CYSGDGRKLSWGLTLRUCALVFTLLMALIYVPHFALLMGLTGLSLGAGLCFLPLSLFHLRL 480

RESULT 10
US-09-972-211-38
; Sequence 38, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkete, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glenda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972.211
; CURRENT FILING DATE: 2001-10-05
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; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 38
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-38

Query Match      99.9%; Score 2746; DB 11; Length 525;
Best Local Similarity 99.8%; Pred. No. 5.1e-253;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVSNKSQAQKMGFMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQ 60
DB 1 MATLLRSKLSNVATSVSNKSQAQKMGFMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQ 60
QY 61 DILKAEPCGDEGAEPVEGDHYQRGSGAPLPSSGKQVGGGEGFGHDKPKITAW 120
DB 61 DILKAEPCGDEGAEPVEGDHYQRGSGAPLPSSGKQVGGGEGFGHDKPKITAW 120
QY 121 AGNVTNAIQGMFVLGFLPYAILHGGYGLFLIIFAAVVCCYTGKILIACLYEENEDGEV 180
DB 121 AGNVTNAIQGMFVLGFLPYAILHGGYGLFLIIFAAVVCCYTGKILIACLYEENEDGEV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRRVNVVAQIIELVMTCILYVVSNGMLMNSFFGLPV 240
DB 181 RVRDSYVAIANACCAPRPTLGGRRVNVVAQIIELVMTCILYVVSNGMLMNSFFGLPV 240
QY 241 KWSIIATAVLLPCAFKXNLKAVSKFSLICTLAHFVINILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAFKXNLKAVSKFSLICTLAHFVINILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTHTIAACVLKGLFALVAY 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTHTIAACVLKGLFALVAY 360
QY 361 TWADETKEVITDNLPGSIRAVVNIPLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFPA 420
DB 361 TWADETKEVITDNLPGSIRAVVNIPLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFPA 420
QY 421 CYSGDGRKLSWGLTLRUCALVFTLLMALIYVPHFALLMGLTGLSLGAGLCFLPLSLFHLRL 480
DB 421 CYSGDGRKLSWGLTLRUCALVFTLLMALIYVPHFALLMGLTGLSLGAGLCFLPLSLFHLRL 480
QY 481 LWRKLLWHQVFPDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525
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Db	481	LWRKLLWHQVFDVAIFVIGGICVSGFVHSLGLEIEAYRTNAED	525
RESULT 11			
US-10-096-625-30			
; Sequence 30, Application US/10096625			
; Publication No. US20040068095A1			
; GENERAL INFORMATION:			
; APPLICANT: Shimkets, Richard A			
; APPLICANT: Taupier Jr, Raymond J			
; APPLICANT: Burgess, Catherine E			
; APPLICANT: Zerhusen, Bryan D			
; APPLICANT: Mezes, Peter S			
; APPLICANT: Rastelli, Luca			
; APPLICANT: Malyankar, Uriel M			
; APPLICANT: Grosse, William M			
; APPLICANT: Alsobrook II, John P			
; APPLICANT: Lepley, Denise M			
; APPLICANT: Spytek, Kimberly Ann			
; APPLICANT: Li, Li			
; APPLICANT: Edinger, Shlomit			
; APPLICANT: Gerlach, Valerie			
; APPLICANT: Ellerman, Karen			
; APPLICANT: MacDougall, John R			
; APPLICANT: Gunther, Erik			
; APPLICANT: Millet, Isabelle			
; APPLICANT: Stone, David J			
; APPLICANT: Smithson, Glenda			
; APPLICANT: Szekeres Jr, Edward S			
; APPLICANT: Ji, Weizhen			
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th			
; FILE REFERENCE: 21402-141 CIP			
; CURRENT APPLICATION NUMBER: US/10/096.625			
; CURRENT FILING DATE: 2002-03-13			
; PRIOR APPLICATION NUMBER: 09/972,211			
; PRIOR FILING DATE: 2001-10-05			
; PRIOR APPLICATION NUMBER: 60/238,325			
; PRIOR FILING DATE: 2000-10-05			
; PRIOR APPLICATION NUMBER: 60/238,323			
; PRIOR FILING DATE: 2000-10-05			
; PRIOR APPLICATION NUMBER: 60/238,400			
; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/238,397			
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; PRIOR FILING DATE: 2000-10-06			
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; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/238,372			
; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/238,383			
; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/238,382			
; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/275,892			
; PRIOR FILING DATE: 2001-03-14			
; PRIOR APPLICATION NUMBER: 60/296,860			
; PRIOR FILING DATE: 2001-06-08			
; NUMBER OF SEQ ID NOS: 200			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 30			
; LENGTH: 525			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-10-096-625-30			

Query Match	99.9%	Score 2746;	DB 15;	Length 525;
Best Local Similarity	99.8%	Pred. No. 5.1e-253;		
Matches 524;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MATLLRSKLSNVATSVSNKSOAKMSGMFARMGQAAATDEEAVGFAHCDDLDFFEHRGLOQM	60
Db	1	MATLLRSKLSNVATSVSNKSOAKMSGMFARMGQAAATDEEAVGFAHCDDLDFFEHRGLOQM	60
QY	61	DILKAEPEPCGDEGAEPVEGDHYQKSGAPLPPSGSKDQVGGGFGGHDGPKITAW	120
Db	61	DILKAEPEPCGDEGAEPVEGDHYQKSGAPLPPSGSKDQVGGGFGGHDGPKITAW	120
QY	121	AGNVTNAIQGMFVLGFLPYAILHGGYLGFLIIPAAVVCCTGKILIACTYEENDEGEV	180
Db	121	AGNVTNAIQGMFVLGFLPYAILHGGYLGFLIIPAAVVCCTGKILIACTYEENDEGEV	180
QY	181	RVRDSYVAIANACCAPRPTLGGRRVAVVQIIELVMTCILYVVVSGNLMYNSFPLPVSQ	240
Db	181	RVRDSYVAIANACCAPRPTLGGRRVAVVQIIELVMTCILYVVVSGNLMYNSFPLPVSQ	240
QY	241	KWSIIATAVALLPCAFKLNKAVSKFSLCTLAHFVINILVIAVCLSRADNWEKVKFY	300
Db	241	KWSIIATAVALLPCAFKLNKAVSKFSLCTLAHFVINILVIAVCLSRADNWEKVKFY	300
QY	301	IDVKFPISIGIIVFSYTSQIFLPSLEGNMOOPSEFHCMMNWTTHIAACVLKGLFALVAYL	360
Db	301	IDVKFPISIGIIVFSYTSQIFLPSLEGNMOOPSEFHCMMNWTTHIAACVLKGLFALVAYL	360
QY	361	TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPFPA	420
Db	361	TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPFPA	420
QY	421	CYSGDRLKSWGLTLRICALVVTLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLHLRL	480
Db	421	CYSGDRLKSWGLTLRICALVVTLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLHLRL	480
QY	481	LWRKLLWHQVFDVAIFVIGGICVSGFVHSLGLEIEAYRTNAED	525
Db	481	LWRKLLWHQVFDVAIFVIGGICVSGFVHSLGLEIEAYRTNAED	525

RESULT 12

US-10-096-625-38

Sequence 38, Application US/10096625

Publication No. US20040068095A1

GENERAL INFORMATION:

APPLICANT: Shimkets, Richard A

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Burgess, Catherine E

APPLICANT: Zerhusen, Bryan D

APPLICANT: Mezes, Peter S

APPLICANT: Rastelli, Luca

APPLICANT: Malyankar, Uriel M

APPLICANT: Grosse, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Lepley, Denise M

APPLICANT: Spytek, Kimberly Ann

APPLICANT: Li, Li

APPLICANT: Edinger, Shlomit

APPLICANT: Gerlach, Valerie

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John R

APPLICANT: Gunther, Erik

APPLICANT: Millet, Isabelle

APPLICANT: Stone, David J

APPLICANT: Smithson, Glenda

APPLICANT: Szekeres Jr, Edward S

APPLICANT: Ji, Weizhen

TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th

FILE REFERENCE: 21402-141 CIP

CURRENT APPLICATION NUMBER: US/10/096.625

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 09/972,211

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/238,325

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 60/238,323

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 60/238,400

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,397

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,401

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,379

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,402

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 30/238,384

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,373

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,372

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,383

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238,382

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/275,892

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/296,860

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 200

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 30

LENGTH: 525

TYPE: PRT

ORGANISM: Homo sapiens

US-10-096-625-30



CURRENT FILING DATE: 2002-03-13
PRIORITY APPLICATION NUMBER: 09/972,211
PRIORITY FILING DATE: 2001-10-05
PRIORITY APPLICATION NUMBER: 60/238,325
PRIORITY FILING DATE: 2000-10-05
PRIORITY APPLICATION NUMBER: 60/238,323
PRIORITY FILING DATE: 2000-10-05
PRIORITY APPLICATION NUMBER: 60/238,400
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,397
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,401
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,379
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,402
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 30/238,384
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,373
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,372
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,383
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,382
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/275,892
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 60/296,860
PRIORITY FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-10-096-625-38

Query Match
Best Local Similarity 99.9%; Score 2746; DB 15; Length 525;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVA:SVNKSQAKSGMFARMGFOAATDEAVGFAHCDDLDFFEHRQGLQM 60
DB 1 MATLLRSKLSNVA:SVNKSQAKSGMFARMGFOAATDEAVGFAHCDDLDFFEHRQGLQM 60
QY 61 DILKAECEPCGDEGAEPVEGDIIHYQRGSGAPLPSSGSKQVGGGFGGHDKPKITAW 120
DB 61 DILKAECEPCGDEGAEPVEGDIIHYQRGSGAPLPSSGSKQVGGGFGGHDKPKITAW 120
QY 121 AGMNVTAIQGMFVLGPLYALHGGYLGFLIIFAAVVCCTGKILIACLYEENDEGEV 180
DB 121 AGMNVTAIQGMFVLGPLYALHGGYLGFLIIFAAVVCCTGKILIACLYEENDEGEV 180
QY 181 RVRDSYVAIANACAPRPTLGRVNVNAQIIEIWMTCILYVVVSGNLMYNSPGLPVSQ 240
DB 181 RVRDSYVAIANACAPRPTLGRVNVNAQIIEIWMTCILYVVVSGNLMYNSPGLPVSQ 240
QY 241 KWSIIITAVLLPCAFILKLVKAVSKFSLCTLAHFVNILIVAYCISRAEDWAEWKVF 300
DB 241 KWSIIITAVLLPCAFILKLVKAVSKFSLCTLAHFVNILIVAYCISRAEDWAEWKVF 300
QY 301 IDVKKFPISIGIIVFSTQIFLPSLEGNMQPSEPHCMWNTHIAACVLKGLFALVAYL 360
DB 301 IDVKKFPISIGIIVFSTQIFLPSLEGNMQPSEPHCMWNTHIAACVLKGLFALVAYL 360
QY 361 TWADETEKVTDLNPGSIRAVNIFLVAKALLSVPLPFFFAVEVLEKSLFOEGSRAFFPA 420
DB 361 TWADETEKVTDLNPGSIRAVNIFLVAKALLSVPLPFFFAVEVLEKSLFOEGSRAFFPA 420
QY 421 CYSQDGRKLSWGLTLRCALVVFLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLPHRL 480

DB 421 CYSQDGRKLSWGLTLRCALVVFLLMAIYVPHFALLMGLTGSITGAGLCFLPLSLPHRL 480
QY 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIYAYRTNAED 525
DB 481 LWRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIYAYRTNAED 525

RESULT 13
US-09-972-211-36
Sequence 36, Application US/09972211
Publication No. US20040048245A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Zerhusen, Bryan D
APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
APPLICANT: Malyankar, Uriel M
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Spytek, Kimberly Ann
APPLICANT: Li, Li
APPLICANT: Edinger, Shlomit
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David J
APPLICANT: Smithson, Glennda
APPLICANT: Szekeres Jr, Edward S
TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides Encoding T
FILE REFERENCE: 21402-141
CURRENT APPLICATION NUMBER: US/09/972,211
CURRENT FILING DATE: 2001-10-05
PRIORITY APPLICATION NUMBER: 60/238,325
PRIORITY FILING DATE: 2000-10-05
PRIORITY APPLICATION NUMBER: 60/238,323
PRIORITY FILING DATE: 2000-10-05
PRIORITY APPLICATION NUMBER: 60/238,400
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,397
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,401
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,379
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,402
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 30/238,384
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,373
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,372
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,383
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/238,382
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/275,892
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 60/296,860
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-211-36

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Query Match          99.7%; Score 2742; DB 11; Length 525;
Best Local Similarity 99.6%; Pred. No. 1.2e-252;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVNKSQAKSGMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQM 60
DB 1 MATLLRSKLSNVATSVNKSQAKSGMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQM 60
QY 61 DILKAEPEPCGDEGAEPVEGDIHYQSGGAPLPSPGSKDOVGGGEGFGHDKPKITAW 120
DB 61 DILKAEPEPCGDEGAEPVEGDIHYQSGGAPLPSPGSKDOVGGGEGFGHDKPKITAW 120
QY 121 AGWNTVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEVV 180
DB 121 AGWNTVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEVV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRVVNAQIIELVMTCTILYVVVSGNLMYNSPFGPLVPSQ 240
DB 181 RVRDSYVAIANACCAPRPTLGGRVVNAQIIELVMTCTILYVVVSGNLMYNSPFGPLVPSQ 240
QY 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
QY 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMWTHIAACVLKGLFALVAYL 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMWTHIAACVLKGLFALVAYL 360
QY 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
DB 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
QY 421 CYSGDGLKSWGLTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLFLHRL 480
DB 421 CYSGDGLKSWGLTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLFLHRL 480
QY 481 LWRKLLHQVFFDVAIFVIGGICSVGFSVHSLGLELIBAYRTNAED 525
DB 481 LWRKLLHQVFFDVAIFVIGGICSVGFSVHSLGLELIBAYRTNAED 525

RESULT 14
US-10-096-625-36
; Sequence 36, Application US/10096625
; Publication No. US20040068095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glenda
; APPLICANT: Szekeres Jz, Edward S
; APPLICANT: Ji, Weizhen
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding TH
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141 CIP
; CURRENT APPLICATION NUMBER: US/10/096,625
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; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 36
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-096-625-36

Query Match          99.7%; Score 2742; DB 15; Length 525;
Best Local Similarity 99.6%; Pred. No. 1.2e-252;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATLLRSKLSNVATSVNKSQAKSGMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQM 60
DB 1 MATLLRSKLSNVATSVNKSQAKSGMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQM 60
QY 61 DILKAEPEPCGDEGAEPVEGDIHYQSGGAPLPSPGSKDOVGGGEGFGHDKPKITAW 120
DB 61 DILKAEPEPCGDEGAEPVEGDIHYQSGGAPLPSPGSKDOVGGGEGFGHDKPKITAW 120
QY 121 AGWNTVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEVV 180
DB 121 AGWNTVTAIQGMFVLGFLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEVV 180
QY 181 RVRDSYVAIANACCAPRPTLGGRVVNAQIIELVMTCTILYVVVSGNLMYNSPFGPLVPSQ 240
DB 181 RVRDSYVAIANACCAPRPTLGGRVVNAQIIELVMTCTILYVVVSGNLMYNSPFGPLVPSQ 240
QY 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
DB 241 KWSIIATAVLLPCAPFLKYLKAVSKFSLCTLAHFVNILVIAYCLSRARDWAEKVKFY 300
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMWTHIAACVLKGLFALVAYL 360
DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMWTHIAACVLKGLFALVAYL 360
QY 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
DB 361 TWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
QY 421 CYSGDGLKSWGLTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLFLHRL 480
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Db 421 CYSGDRLKSWGLTLRCALVWFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLPSLFLHRL 480  
 Qy 481 LMRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525  
 Db 481 LMRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525

RESULT 15

US-09-972-211-32  
 ; Sequence 32, Application US/09972211  
 ; Publication No. US20040048245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shimkets, Richard A  
 ; APPLICANT: Taupier Jr, Raymond J  
 ; APPLICANT: Burgess, Catherine E  
 ; APPLICANT: Zerhusen, Bryan D  
 ; APPLICANT: Mezes, Peter S  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Malyankar, Uriel M  
 ; APPLICANT: Grosse, William M  
 ; APPLICANT: Alsobrook II, John P  
 ; APPLICANT: Lepley, Denise M  
 ; APPLICANT: Spytek, Kimberly Ann  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: MacDougall, John R  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Stone, David J  
 ; APPLICANT: Smithson, Glennda  
 ; APPLICANT: Szekeres Jr, Edward S  
 ; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th  
 ; TITLE OF INVENTION: Methods Of Using The Same  
 ; FILE REFERENCE: 21402-141  
 ; CURRENT APPLICATION NUMBER: US/09/972,211  
 ; PRIOR FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,325  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,323  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,400  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: 60/238,397  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,401  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,379  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,402  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 30/238,384  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,373  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,372  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,383  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,382  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/275,892  
 ; PRIOR FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: 60/296,860  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 32  
 ; LENGTH: 525  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-972-211-32

Query Match 99.6%; Score 2739; DB 11; Length 525;  
 Best Local Similarity 99.6%; Pred. No. 2.4e-252;  
 Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 MATLLRSKLSNVATSVSNKSOAKXSGMFAEMGQAATDEEAVGFAHCDDLDDEHROGLQM 60  
 Db 1 MATLLRSKLSNVATSVSNKSOAKXSGMFAEMGQAATDEEAVGFAHCDDLDDEHROGLQM 60  
 Qy 61 DILKAEPCGDEGAEPVEGDIIHYQSGCAPLPPSGSKDQVGGGEGFGHDKPKITAW 120  
 Db 61 DILKAEPCGDEGAEPVEGDIIHYQSGCAPLPPSGSKDQVGGGEGFGHDKPKITAW 120  
 Qy 121 AGNVTNAIQGMFVLGLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEV 180  
 Db 121 AGNVTNAIQGMFVLGLPYAILHGGYLGFLIIIFAAVVCCTGKILIIACLYEENEDGEV 180  
 Qy 181 RVRDSYVAIANACAPRFPPTLGRVNVNAQIIELVMTCTILYVVVSGNLMVNSPGLPVSQ 240  
 Db 181 RVRDSYVAIANACAPRFPPTLGRVNVNAQIIELVMTCTILYVVVSGNLMVNSPGLPVSQ 240  
 Qy 241 KWSIIATAVLLPFCALFKNLKAVSKFSLCTLAHFVINILVIAYCLSRARDMAWEKVFY 300  
 Db 241 KWSIIATAVLLPFCALFKNLKAVSKFSLCTLAHFVINILVIAYCLSRARDMAWEKVFY 300  
 Qy 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNTHIAACVLKGLFALVAYL 360  
 Db 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNTHIAACVLKGLFALVAYL 360  
 Qy 361 TWADEKTEITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPA 420  
 Db 361 TWADEKTEITDNLPGSIRAVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPA 420  
 Qy 421 CYSGDRLKSWGLTLRCALVWFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLPSLFLHRL 480  
 Db 421 CYSGDRLKSWGLTLRCALVWFTLLMAIYVPHFALLMGLTGSITGAGLCFLPLPSLFLHRL 480  
 Qy 481 LMRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525  
 Db 481 LMRKLLWHQVFFDVAIFVIGGICSVSGFVHSLGLEIEAYRTNAED 525

Search completed: November 8, 2004, 18:59:58  
 Job time : 183 secs

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Db 164 ----QAVLGNLVLCGVGILSTPYAAKEGGWGLMILFVYGLLSFYTGILLRYCLDSESD 219  
QY 176 DGEVVRVDSVAIANACCAFRPPTLGRVNVNAQIIELVMTCLYVYVSGNLMYNSFPFG 235  
Db 220 -----LETYPDIGQAA-----FGTGTGRIFVSIYLYLELYACCVYIILBSDNLSLYPN 268  
QY 236 LPVS-----QKSWSIATAVLLPCAFNLKNLKA VKFSLLCTLAHFVNILVIAVCLSL 287  
Db 269 AALSIGGQOLDARHLFALLTTLAVLPTWLRDLSVLYS-----AGGVIASVLVLCCL- 322  
QY 288 RARDWAW-----EKVKFY-----IDVKKFPPIGIIIVFSYTSQIFLPSLEGNMQOPSEFHC 338  
Db 323 -----FWLGVDEVGISKGTTLNLSTPLVAIGLYGYCSGHAVFPNITYSMKAPSYPA 377  
QY 339 MNWTHIAACVL--KGFALVAYITWADEKTEVITDNLPGSI-----RAVNNIFLVAKALL 392  
Db 378 VL-LTCFGICTLMTAGV-AVMGYTMFGESTQSQTNLNLPQDLIATKIAVWTTLIPSRHR 435  
QY 393 SYPLPFFFAAVEVLEKSLFQEGSRAPFPACYSGDGRKLSW-GLTLRCALVYVFTILMAIYVP 451  
Db 436 SH-----WYAGIRTLTLLVFTSTLLVGLAIP 459  
QY 452 HFALLMGITGSLTGAGLCFLPLSLFHLRLLRKLLWQHVPFDVAIFVIGGICSVSGFVHS 511  
Db 460 FFGVLMSLIGSLTLMVLTLLIPACFLSIVRKVYPTQVMLCVLIIIVGAISSVIGSYS 519  
QY 512 LEGLIB 517  
Db 520 LSKIVE 525

## RESULT 5

T48239  
hypothetical protein T7H20.230 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48239  
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: 224488  
A:Accession: T48239  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-543 <BEV>  
A:Cross-references: UNIPROT:Q9LZL4; EMBL:AL162508  
A:Experimental source: cultivar Columbia; BAC clone T7H20  
C:Genetics:  
A:Map position: 5  
A:Introns: 74/2; 168/1; 234/1; 242/1; 302/1; 375/2; 420/3; 476/1; 490/3; 511/3  
A:Note: T7H20.230  
C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 11.58; Score 317; DB 2; Length 543;  
Best Local Similarity 24.7%; Pred. No. 1.7e-18;  
Matches 102; Conservative 76; Mismatches 169; Indels 66; Gaps 12;

QY 124 NVTNAIQCMFVLGYPAILHGGYLGFLIIFAAVVCCYTGKILIIACLYEBNEDEGEVVR 183  
Db 167 NGTNVLCGLITMPYAIKESWGLPILLFPGVITCYGVLMKRCI--ESSFG----- 218  
QY 184 DSVVAIANACCAFRPPTLGRVNVNA-QIIELVMTCLYVYVSGNLMYNSFPGLPYVSKS 242  
Db 219 -----IOTYPDIGQAFGIDTSSIRGVVPCVEYIIMSDNLGLFPNVLSIAS 267  
QY 243 -----WSIATAVLLPCAFNLKNLKA VKFSLLCTLAHFVNILVIAVCLSRARDW- 292  
Db 268 GISLDSQIIFALLTLLVFTVWMLKLSLSYVSGVGLASILLGI-----CLF-----WV 318  
QY 293 -AMEKVKFY-----IDVKKFPPIGIIIVFSYTSQIFLPSLEGNMQOPSEFHCMMWTHIA 346  
Db 319 GAVDGI GFHATGRVFDLSNLPVTIGIFGCGYSGHSPFNISYSSMKDPSRFPFLVIVICPSF 378  
QY 347 ACVLKGLFALVAYITWADEKTEVITDNLPGSI--RAVNNIFLVAKALLSYPLPFFFAAVEV 404

Db 379 CTVLYIAVAVCGYTMGEAVEVSCQFTLNMPEKHFPPSKVAVWTAIVITPMTKYALTITPIVMS 438  
QY 405 LEKSLFQEGSRAPFPACYSGDGRKLSWGLTL--RCALVYVFTILMAIYVPHFALLMGLTGS 462  
Db 439 LEEI-----PTAKMSRGVSILFRMTLVTSTLWALSVPFFFAIVAALIGS 484  
QY 463 LTGAGLCFLPLSLFHLRLLRKLLWQHV---PFDVAIFVIGGICSVSGFVHSL 512  
Db 485 FLAMLVALIFPCLCYLSILKGLKLSNTQIGLCIFIIIVFGVSGCCGTYSALSRL 537

## RESULT 6

H88022  
protein T27A1.5 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H88022  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustli.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_el  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an  
A:Accession: H88022  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-449 <STO>  
A:Cross-references: UNIPROT:O17275; GB:chr\_II; PIDN:AB71045.1; PID:g2429516; GSPDB:GN00  
C:Genetics:  
A:Gene: T27A1.5  
A:Map position: 2  
C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 11.1%; Score 306; DB 2; Length 449;  
Best Local Similarity 23.4%; Pred. No. 1.1e-17;

Matches 107; Conservative 91; Mismatches 219; Indels 40; Gaps 15;

QY 85 YORGSGAPLPSPGSKDQVGGGEGFG--HDKPKITAWAGNVTWAIQGMFVLGYPAIL 142  
Db 6 YDTARGNELPLRGSHQPTMGEMFASRVDRSRSITADQALHMKVXMTGTGMLSLPLAFK 65  
QY 143 HGG-YLGLFLIIFAAVVCCYTGKILI-----ACLVEENDEGEVVRVRSYVAIANACCAP 196  
Db 66 HSGIWLGLILLCIFCLICIYCTRQLIFQGHYITFKRQRMIDYANMRSAVELGPAWIRG 125  
QY 197 RPTTLGGRVNVNAQII-ELVMTCLYVYVSGNL--MYNSFPCLPVSKSWSIIATAVLLP 253  
Db 126 H-GYLFQKQWNNMFVAQFGCCVYFVEMADNLKQFFDQTSIIHISOAGWIAL---LLIP 181  
QY 254 CAFLNKLKAVSKFSLCTLAHFVNILVIAVCLSRARDW-AMEKVKFVIDVKKFPISIGI 312  
Db 182 ISALCTIRELKALAPLAAVANFVIIAVVIVLADLFSQWQLDSLPAFPAVENTPLFPGT 241  
QY 313 IVFYSYTSQIFLPSLEGNMQOPSEF---HCMNNWTHIAACVLKGLFALVAYITWADEKTEV 369  
Db 242 VMFAEGVAVVLPPIENQNEPIHITPNGVLTSCILVLYVMTVGFPGFLRYGNDIDKT 301  
QY 370 ITDNLPGS-IRAVNNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRA-FFPACYSGDGR 427  
Db 302 LTNLPLPFPFYQAIKMFVLCILVSYPLQFYVPMVERVEKWKRVKVEAKQBFMIYA---- 357  
QY 428 LKSWGLTLRCALVWFTLMAIYVPHFALLMGLTGLTGAIGLCFLPLPSI:PHRLRLW----- 482  
Db 358 IRFGVLTCA-----MAQIIFHALFISLVSVAGTSITLVFPFPIELLCYSKQEL 410  
QY 483 RXLLMHQVFFPDVAIFVIGGICSVSGFVHSLGLEIAY 519  
Db 411 TKWVMIR---NIGLMAFAMVGFTTGTVASMQIIEAF 444

## RESULT 7

T26845

hypothetical protein Y43F4B.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T26845  
 R:Matthews, L.  
 submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z20276  
 A:Accession: T26845  
 A:Status: preliminary; translated from GE/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-607 <WIL>  
 A:Cross-references: UNIPROT:O45936; EMBL:AL021481; PIDN:CAA16336.1; CESP:Y43F4B.7  
 A:Experimental source: clone Y43F4B  
 C:Genetics:  
 A:Gene: CESP:Y43F4B.7  
 A:Introns: 53/3; 80/3; 110/2; 141/2; 169/3; 229/1; 261/3; 300/2; 320/2; 355/3; 377/1; 411

Query Match 10.8%; Score 298; DB 2; Length 607;  
 Best Local Similarity 22.8%; Pred. No. 7.5e-17;  
 Matches 100; Conservative 94; Mismatches 186; Indels 58; Gaps 17;

QY 72 DEGAEPVEGDIHQVQSGAPLPSPGSKDQVGGGEGFGHDKPKITAEAGWNTVNAIQG 131  
 DB 13 DNEFEAPGDIHQVQSGAPLPSPGSKDQVGGGEGFGHDKPKITAEAGWNTVNAIQG 64  
 QY 132 MFVLGLPYAILHGG-YLGLFLIIPAAVCCY-TGKILIACLYEENDEGEVVRVD--SYV 187  
 DB 65 TGLSLPLAFKHSGLFLGLILTLVLCILICLYCMQVFAAFHFCNRRG-----RDLDYA 119  
 QY 188 AIANAC--CAPRPFTLGG---RVNVAQII-ELWMTCILYVVVSGNL--MYNSFPGLPV 238  
 DB 120 NIMRGAVEMGPWKIKNGYFFKQIVNVMFISQLGFCVYVFMADNLEDFFNNNTSIHL 179  
 QY 239 SQKSWSIATAVLLPCAFKLNKLVKSPSLTCTLAHFVINILVIAVCLSRARDWAEKVK 298  
 DB 180 SKAVMMLLLIPMLISICIRSLSLAPFAANVAVVAVVLFPLSLRPLIS--SLP 237  
 QY 299 FYIDVKFPISIGIIVSYTSQIFLPSLEGNMQOPSEFFHCMWTHI--AAC-VLXGLFA 355  
 DB 238 WFGKATDLPLFFGVMAFEGVAVIMPIENRQSP---HAFISWGVLSNCSCLVLAIFS 294  
 QY 356 LV---AYLTWADETKEVITDNLPQS--IRAVVNIPLVAKALLSYPLPFFFAAVEVLEKSL-- 409  
 DB 295 VTGFYGLSLGNDVKDTATLNPPTFYQIKLMFVACIMISYPLQYVPMERIEKWITR 354  
 QY 410 ---FQEGSRAPFPACYSQDGLKSWGLTLRCALVVFLLMAIYVPHALLMGLTGSILTA 466  
 DB 355 KIPVDKQTLTYIARYSG-----VILTCAIAELIPIHLFISLIGAFSGA 399  
 QY 467 GLCLPLPSLPHRLLRWK 484  
 DB 400 SMALLFPFCIELLTSYAK 417

RESULT 8  
 T05653  
 amino acid transport protein homolog F22113.20 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T05653  
 R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
 submitted to the Protein Sequence Database, February 1999  
 A:Reference number: Z15420  
 A:Accession: T05653  
 A:Molecule type: DNA  
 A:Residues: 1-436 <BEV>  
 A:Cross-references: UNIPROT:Q9SVG0; EMBL:AL035539  
 A:Experimental source: cultivar Columbia; BAC clone F22113  
 C:Genetics:  
 A:Map position: 4  
 A:Note: F22113.20  
 C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 10.7%; Score 295.5; DB 2; Length 436;  
 Best Local Similarity 25.8%; Pred. No. 8.2e-17;  
 Matches 116; Conservative 79; Mismatches 188; Indels 67; Gaps 14;

QY 93 LPPSGSKDQVGGGEGFGHDKPKITAEAGWNTVNAIQGMFVLGLPYAILHGGYL-GLFL 151  
 DB 16 IPPARED-----SPILGKGPPLSSQFKTANVFIIVGAGVLGLPYAFKRTGMLMGVLL 70  
 QY 152 IIFAAVCCYTGKILIACLYEENDEGEVVRVRSYVAIANACAPRPTLGGRVNVAQI 211  
 DB 71 LVSVSVLTHHCHMMLLVYTRRKLDSEFNAGISKIGSGDLGFAVCG-----SLGRIVVDLFI 126  
 QY 212 IELVMTCILYVVVSGNLMYN--SPGLP-----VSQKS---WSIATAV- 250  
 DB 127 LSQAGFCVGYLIFITGTLANLSDPESSTLRHQFTRLGSEBFLGVSSKSLVINGCFPPQLG 186  
 QY 251 LLPCAFLKLNKAVKFSLLCTLAHFVINILVIAVCLSRARDWAEKVKFIDVKKPPI 310  
 DB 187 LNSIKTLTHLAPLSIFADIVDLGAMAVVIVEDSMILKQR-----PDVVAFGMSLFLYGM 242  
 QY 311 GLIIVSYTSQIFLPSLEGNMQOPSEFFHCM-----NWTIIAACVLKGLFALVAYLTWA 363  
 DB 243 GVAVYFEGVGMVLPSEMKDKDKFKVLAGMGFISLIYIA-----FGILGYLAFG 295  
 QY 364 DETKEVITDNL-PGSIRAVNIFLVAKALLSYPLPFFFAAVEVLEKSLFQEGSRAFPAC 422  
 DB 236 EDTWIDITANLGLAVSTVVLGGLCINLFTFFPLMNPVEIVE-----RRFSRGM 347  
 QY 423 SGDRKSKWGLTLRCALVVFLLMAIYVPHALLMGLTGSITGAGLCFLPLPSLHLLW 482  
 DB 348 S-----AW---LRWLVLAVTLVAFVNFADFSLVGSSTCCVGLGVLPALFHLVFK 398  
 QY 483 EKLWHQVFFDVAIFVIGGICVSGVGHSL 512  
 DB 399 EEMGLQWSSDTAVLGLVLAWSGTWSSL 428

RESULT 9  
 T06737  
 hypothetical protein F28P10.190 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T06737  
 R:Quetier, F.; Choissin, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigou  
 submitted to the Protein Sequence Database, April 1999  
 A:Reference number: Z15793  
 A:Accession: T06737  
 A:Molecule type: DNA  
 A:Residues: 1-571 <QUE>  
 A:Cross-references: UNIPROT:Q9SV32; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.190  
 A:Experimental source: cultivar Columbia; BAC clone F28P10  
 C:Genetics:  
 A:Gene: ATSP:F28P10.190  
 A:Map position: 3  
 A:Introns: 63/2; 159/1; 230/3; 238/3; 299/1; 372/2; 417/3; 470/1; 503/1

Query Match 10.4%; Score 285; DB 2; Length 571;  
 Best Local Similarity 23.5%; Pred. No. 8.5e-16;  
 Matches 99; Conservative 84; Mismatches 164; Indels 74; Gaps 15;

QY 66 EGEPGCD---EGAPVEGDHYQSGCAPLPSPSGSKDQV-----GGGEGFGHDKP 114  
 DB 104 ESLPCVTPPLLEDEAP-----KHLSTHLLPSKPSMVMVSHDMGINSNDSFG----- 153  
 QY 115 KITAEAGWNTVNAIQGMFVLGLPYAILHGGYGLGLIIFAAVCCYTGKILIACLYEEN 174  
 DB 154 ----QAVLGVNVLGCGVIGLSTPYAVKEGGMGLIILFAFGILCFYTGLLRYCL-DSH 207  
 QY 175 EDGEVVRVRSYVAIANACAPRPTLGGRVNVAQIITELVMTCILYVVVSGNLMYNSFP 234  
 DB 208 PDVQ-----TYPDIGHAA-----FGSTGRILVSVILNELYAMSVVEYILLEDNLSNFP 257  
 QY 235 GLPVS-----QKSWSIATAVLLPCAFKLNKLVKAVSKFSLCTLAHFVINILVIAVCL 286



Db 258 NASLSIGGFHLDAPLFAALLTTLAVLPVWLRDLVLSVYS-----AGGVIASVLVWLCL 312  
QY 287 SRARDWAW--EKVKFY-----IDVKFPISIGLIVFSYTSQIFLPSLEGNNQCPSEFHC 339  
Db 313 F----WVGLVDVGHSGTLPNLATLPVSVGLVGYCYSGHGVFNITYSWAKPSQSAV 368  
QY 340 MNWTHIAACVLKGLFALVAYITWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLPFF 399  
Db 369 LIASFGICTLMYAGVAVMGVSMFGESTESQFTNLNLPQDLVA-SKIALWTTKRESYALTLS 427  
QY 400 AAVEVLERSLFOEGSRAPFPACYSQDGLKSGWGLTRCALVVFILLMAIYVPHFALLMGL 459  
Db 428 PVMSLEB-----LIPSNY---GKSRFYAIRSALAISTLLVGLAIPFPFNLLSL 475  
QY 460 T 460  
Db 476 T 476

## RESULT 10

Ts1506  
Hypothetical protein F5E19.80 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: Ts1506  
R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew  
submitted to the Protein Sequence Database, August 2000  
A/Reference number: Z25394  
A/Accession: Ts1506  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-426 <SAT>  
A/Cross-references: UNIPROT:Q9LPE3; EMBL:AL391147  
A/Experimental source: cultivar Columbia; BAC clone F5E19  
C/Genetics:  
A/Map position: 5  
A/Introns: 48/1; 247/3  
A/Note: F5E19.80  
C/Superfamily: Arabidopsis amino acid transport protein I

Query Match 9.9%; Score 272; DB 2; Length 426;  
Best Local Similarity 24.3%; Pred. No. 7.3e-15;  
Matches 100; Conservative 75; Mismatches 185; Indels 52; Gaps 10;  
QY 124 NVTNAIOGMFVLGYPYALLHGGYLGLELIIFAAVCCYCTGKILLIACLYEENEDGEVVR 183  
Db 41 NWGMLIGLGOLSPYAVESGGWMSIFLLISFGLTITTYTSHLGKCIIRNPKS----- 93  
QY 184 DSYVAIANACCAPRFTLGRVNVNVAQIIELVMTCILYVVVSGNLMYNSPPG-----L 236  
Db 94 KXSVDIGYSA---FGRHGRLLIVCLFYILEIFMALVSYTISLHDNISAAFPATFSNHGF 149  
QY 237 PVSOKSWSIATAVLLPCAFKLNKAVKFSLLCTLAHFVNILVIACTLSRARDWANEK 296  
Db 150 PAAK--UTAVAVATALPSLWIRDSSISFLSSGILMSAIFGSVVYTAIFGG----- 200  
QY 297 VKFYIDVKKFPI-----SIGIIVFSYTSQIFLPSLEGNNQCPSEFHCMMNWTTHAAC 348  
Db 201 ---VIDDGKIPVLENIPTVSGIYLSFGHIVFNFNLYTSMKDPKFKVSIVSFATVT 257  
QY 349 VLKGLFALVAYLTWADETKEVITDNLPGSIRAVNIFLVAKAL---LSYPLPFAAVEVL 405  
Db 258 ALYGALAITGAKMFGPSVNSQITLSLPKHL-VVTKIALMATVLTPTMTKYALEPAPLAIQL 316  
QY 406 EKSLFOEGSRAPFPACYSQDGLKSGWGLTRCALVVFILLMAIYVPHFALLMGLTSLTG 465  
Db 317 ERSI-----PSTWDTKLVARGL-MGSALLNVILALATVPYFGVLSLTSLVLS 366  
QY 466 AGLCFLPLSPHLRLRLKRLMHWQVDFVAIFVIGGICSVSGFVHSLGLEIEA 517  
Db 367 VTIATVLPESAFYLKICWDGMTKTRAANLGVVLGVLCVGLSGFESSKLLVVK 418

## RESULT 11

JC7961  
Proton-coupled amino acid transporter 2 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 25-Aug-2003 #sequence\_revision 25-Aug-2003 #text\_change 15-Sep-2003  
C/Accession: JC7961  
R/Chen, Z.; Kennedy, D.J.; Wake, K.A.; Zhuang, L.; Ganapathy, V.; Thwaites, D.T.  
Biochem. Biophys. Res. Commun. 304, 747-754, 2003  
A/Title: Structure, tissue expression pattern, and function of the amino acid transport  
A/Reference number: JC7961; PMID:12727219  
A/Accession: JC7961  
A/Molecule type: mRNA  
A/Residues: 1-481 <CHE>  
A/Experimental source: (Lung)  
C/Comment: This transport protein is a second member of H+-coupled, pH-dependent, Na+-i  
sport not only from one cellular compartment to another (across plasma membranes) but a  
C/Genetics:  
A/Gene: pat2  
A/Map position: 10q22  
C/Keywords: amino acid transport system; PAT2

Query Match 9.2%; Score 252; DB 2; Length 481;  
Best Local Similarity 21.9%; Pred. No. 3.9e-13;  
Matches 114; Conservative 89; Mismatches 203; Indels 114; Gaps 22;  
QY 60 MDILKAEGPCGDGEGAEAPVEGDHYRQSGAPLPSPSGSKDQ-----VGGGGEFGHDK 113  
Db 1 MSVTKSAGSP---QVAATVKLDL-----VSFPESAKKVSQDPNPVNGSSSESSEKT 49  
QY 114 PKITAEAGWNTNALQGMFVLGYPYALLHGGYLGLELIIFAAVCCYCTGKILLIAC----- 169  
Db 50 KGITGFQTLVHLVKGNMGTGILGLPLAVNAGILMGP-SLLVMGLIACHMHLVRCAGR 109  
QY 170 -LYEENED---GEVV-----VRDSYVAIANA---CCAPRPPTLG 202  
Db 110 FCHRLNKPFMDYGDVTWHLGLASSPNTWLQSHAHWGHAVSFLLIVTQLGFCVV----- 162  
QY 203 GRVV---NVAQIIELV-----MTCILYVVVSGNLMYNSPPGLPVSOKSWSIAT 248  
Db 163 -YIVFLADNLKQVAVNSNTTISCHKNETVTLTPTIDSRLYMLAF--LP----- 208  
QY 249 AVLLPCAFKLNKAVKFSLLCTLAHFVNILVIACTLSRARDWANEKVFIDVKKPPI 308  
Db 209 -VLGLLVFIRNLRVITISLLANVMSLVSLVIGQYIIQGPDPDS--QLPLVASWKTYP 265  
QY 309 SIGIIVFSYTS-QIFLPSLEGNNQCPSEFHCMMNWTTHAACVLKGLFALV---AYLTWAD 364  
Db 266 PFGTAIFSGESIGVLP-LENKKDARRPPTILS---LGMSIITTLTYIAIGALGYLRFCD 321  
QY 365 ETKEVITDNLPGS-IPAVNIFLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFPACYS 423  
Db 322 DIKASITLNLPCWLYQSVKLLYVVGILCTHALQFYVPAEIIIPLAVSQVS----- 372  
QY 424 GDGRLLKSWG---LTLRCALVVFILLMAIYVPHFALLMGLTSGLTGAGLCFLPLSPHLR 479  
Db 373 -----KRWALPVDLSIRLALVCVTCMLAILPRDLVLVSLVSGSVSSSALALIPLLEV 427  
QY 480 LLWRK-LLWQHVPFVAIFVIGGICSVSGFVHSLGLEIEA 518  
Db 428 TTYGEGMSPLTIKDALISILGFMGVVGTYYQALDELIRS 467

## RESULT 12

S55188  
Hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae)  
N/Alternate names: hypothetical protein U1409; hypothetical protein YJR83.4  
C/Species: Saccharomyces cerevisiae  
C/Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C/Accession: S55188; S57016  
R/de Haan, M.; Smits, P.H.M.; Grivell, L.A.  
submitted to the EMBL Data Library, May 1995  
A/Reference number: S55183

A:Accession: S55188  
A:Molecule type: DNA  
A:Residues: 1-602 <DB>  
A:Cross-references: UNIPROT:P47082; EMBL:X87611; NID:G854567; PIDN:CAA60922.1; PID:G854567  
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.  
submitted to the Protein Sequence Database, September 1995  
A:Reference number: S56771  
A:Accession: S57016  
A:Molecule type: DNA  
A:Residues: 1-602 <ZAG>  
A:Cross-references: EMBL:Z49501; NID:G1015619; PIDN:CAA89523.1; PID:G1015620; MIPS:YJPR00  
A:Cross-references: SGD:S0003761  
A:Map position: 10R

Query Match 8.8%; Score 241; DB 2; Length 602;  
Best Local Similarity 24.2%; Pred. No. 4.2e-12;  
Matches 114; Conservative 85; Mismatches 179; Indels 94; Gaps 22;

QY 89 SGAPLPSPGSKDQV---GGGGEFGHDKPKI-----TAWAGWV 125  
DB 158 SGTSLRPTASITENMWSGGARRFTNDVDSIVVVRGVDGKVVTLLAGOSTAPOTIFNS 217  
QY 126 TNAIQMFVLGLPYAILHGGY-LGL-PLIIFAAVCCYTGKILIACLYEENEDGEVVRV 183  
DB 218 INVLIIGLLALPLGLKYAGWVIGLTLAIFALATFC-TAELLSRCL---DTPDTLI--- 270  
QY 184 DSVVAIANACCAPRFTPLTGGRVNVAQIIELVMTCLIVVYVSGNLMYNSPPGLPVSQKSW 243  
DB 271 -SYADLGAA---FGTKGRALISALTDLGSGVSLVILFGDSLNALFP--QYSTTF 323  
QY 244 SIATAVLLPCAFILKLVKAVSKFSLCTLAHFVNILVIAYC-----LSARDW 292  
DB 324 KIVSFFIVTPVPFIP-LSVLSNISLGLILS-TTGTVLVICCCGLYKSSSPGSLVNPMTS 381  
QY 293 AWEKVFIVDKKPPISIGIIVFSTQIFLPSLEGNNQOPSEFFHCHMMWTHIAACVLKG 352  
DB 382 MWP-----IDKHCLSIGLISACWGHAVFNLKTDHDPKDFKDLCTYKITSVTDI 436  
QY 353 LFALVAVLTWADETKEVITDN-----LPGSIRAVNVNIFLVAKALLSYPLPFAAV 402  
DB 437 GTAVIGFLMFGNLVKDEITKNVLLTEGVPKPVYGLISALMTIIPAKTPLN-ARPIVSVL 495  
QY 403 EVL-EKSLFQSGRAFPACVSGDGLKSNGLTL--RCALVWFTLLMAIYVPHFALLMGL 459  
DB 496 DVLNVQVHIDEAASAI-----KRAAKGLQVNFIRFNVVFLVIAINFPEDKII-- 545  
QY 460 TGSILTGAGLCF---LLPSLPHLRL-----MRKLLMH-QVFFDVAIFVIG 500  
DB 546 --AFLGAGLCCTICLLPCWFLALCKTIKPVWVACHVTCISVVLSTLG 595

RESULT 13  
T49959  
Hypothetical protein F8M21.130 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T49959  
R:Sevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 224493  
A:Accession: T49959  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-423 <BE>  
A:Cross-references: UNIPROT:Q9LXF8; EMBL:AL333993; GSPDB:GN00063; ATSP:F8M21.130  
A:Experimental source: cultivar Columbia; BAC clone F8M21  
C:Genetics:  
A:Gene: ATSP:F8M21.130  
A:Map position: 5  
A:Introns: 48/1; 251/3  
C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 8.6%; Score 236; DB 2; Length 423;  
Best Local Similarity 23.9%; Pred. No. 7.2e-12;  
Matches 99; Conservative 82; Mismatches 172; Indels 62; Gaps 17;

QY 127 NAIQGMFVLGLPYAILHGGVGLFLIIFAAVCCYTGKILIACLYEENEDGEVVRVDSY 186  
DB 44 NALSGVILSVPYALASGGWLSLILFTVAITFYCAILIKRCM-----ENDPLLSY 96  
QY 187 VAIANACCAPRFTPLTGGRVNVAQIIELVMTCLIVVYVSG---NLMVN-----SFGPLPVS 239  
DB 97 PDICVKA---FGNTGRVIVSIFMNLLEYLVATSVFLIEGDNLNKLFNSVGLNFMGLEFQ 152  
QY 240 QKSWSIITATA-VLPCAFILKLVKAVSKFSLCTLAHFVNILVIAYCLSRARDWAMEKVK 298  
DB 153 GKQFIIWALIIILPSVWLDNMRILSVSASGVPASGVILASIPSV-----CAFEGVG 205  
QY 299 F-YIDVKKFPI-----SIGIIVFSTQIFLPSLEGNNQOPSEPH-----CMNWTHIAA 347  
DB 206 FKNDSEVRLNGVATSVSLVAFPCYCAHPVPTLTYSKMKRQSFNSVMIICFTICTFIYA 265  
QY 348 CVLKGFLFALVAYLTWADETKEVITDNLP-GSIRAVNVNIFLVAKALLSYPLPFAA-AVEVL 405  
DB 266 SV-----AVLGYLMYGSVDVESQITNLFTDKLSKVAIW---TTLVNPFAKALMTPTI 316  
QY 406 EKSLFQSGRAFPACVSGDGLKSNGLTLRCALVWFTLLMAIYVPHFALLMGLTGSLTG 465  
DB 317 IDAKRSRFRVL-----PNKASGFLSTILVTSNVIVALLPFPGLMSLVGAFLS 368  
QY 466 AGLCFLLPSLPHLRLKRLMHQVFDVAIFVIGGICSVSGFVHSLGLEIAYR 520  
DB 369 ASASVILPCLCYLKISGK---YORLGFETLVI--GI-TLTGIYVWITGTQYAVK 417

RESULT 14  
T34016  
Hypothetical protein Y4C6B.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T34016  
R:Layman, D.; Graves, T.; Yeakum, M.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y4C6B.  
A:Reference number: Z21460  
A:Accession: T34016  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-484 <LAYS>  
A:Cross-references: UNIPROT:Q9UAZ9; EMBL:AF125971; PIDN:AAD14765.1; GSPDB:GN00022; CESP:  
A:Experimental source: strain Bristol N2; clone Y4C6B  
C:Genetics:  
A:Gene: CESP:Y4C6B.2  
A:Map position: 4  
A:Introns: 97/2; 272/3; 312/1; 403/1; 450/2  
C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 8.1%; Score 223; DB 2; Length 484;  
Best Local Similarity 22.5%; Pred. No. 1e-10;  
Matches 101; Conservative 91; Mismatches 179; Indels 78; Gaps 20;

QY 112 DKPKITAWAGWNVNVAIQGMFVLG-----LPYAILH-GGYLGLFLIIFAAWCCY 161  
DB 2 DQPHIN-EKGMISI--LVTAFLIVGETAGGGLIAPLTAIVSTGAVTGAFLLVAAVCTY 57  
QY 162 TKIL-----TACLYEENEDGEVVRVDSYVAIANACCAPRFTPLTGGRVNVAQIIELV 215  
DB 58 TGIILAEWNTILQELYPEYRD-----HCRKPYAMGLRAIGPKFAHFVSAIMQVTOFTAV 113  
QY 216 MTCILVVVSVGNLMYNSPPGLPVSQKSWSIATATVLLPCAFILKLVKAVSKFSLCTLAHF 275  
DB 114 VFVLLAANGENLHANP-GTHVSCYMLIVGLLVFFFTLPKSPKDF-WVAVVAAIMST 171  
QY 276 VINILVIAYCLSRARDW-AWEKVFY--IDVKKFPISIGIIVFSTQIFLPSLEGNNQO 332

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Db 172 TISVLLIIF--GTQVDYEVCHKEVFPSPFNESKTLMSFGTINFSYGHGHCAPTTHQDMKK 229
QY 333 PSEHFMNWNTHIAACVLKGLF-----ALVAYLTWADETKEVITDNLPG-SIRAVVNIFLV 387
Db 230 PHHF-----SRSIITAFIIFIPYLPVSMGYSYVYVSSLTDSIIPSIQININQITVINILIS 285
QY 388 AKALLSYPLPFAAIVELEKSLFQBGSRAPFPACYSYDGRKLSWGLRLRCALVVFTLL-M 446
Db 286 LHSVLAITITNPLNQBEFEL--NMSHDF-----GWQRIVARALVMLSVVFV 331
QY 447 AIYVPHFALLMGLTSGLTGAGLCFLPLSLFHLRLW-----RKLWHQVFFD-- 493
Db 332 AESVENFGVLLDLVGGSTITMMLWPIVFNALTTIKKKENKDNEEKLTIKEIFQNSD 391
QY 494 -----VALFVI--GGICVSGFVHSL 512
Db 392 KIKLANILILVFAIFGGAATTSAMQTM 420

RESULT 15
JC7626
amino acid transport system N transporter, SN2 - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7626
R:Nakanishi, T.; Sugawara, M.; Huang, W.; Martindale, R.G.; Leibach, F.H.; Ganapathy, M.
Biochem. Biophys. Res. Commun. 281, 1343-1348, 2001
A:Title: Structure, function, and tissue expression pattern of human SN2, a subtype of c
A:Reference number: JC7626; MUID:21139776; PMID:11243884
A:Contents: Liver cell line HepG2
A:Accession: JC7626
A:Molecule type: mRNA
A:Residues: 1-472 <NAK>
A:Cross-references: UNIPROT:Q96PQ4; GB:AF276889; GB:AF196972
C:Comment: This SN2, an amino acid transporter, mediates Na+-coupled transport of system
line, and glycine. The transport function of SN2 is pH-dependent and Li+-tolerant.
C:Genetics:
A:Gene: sn2
A:Map position: X p11.23
C:Keywords: amino acid transport; transport system

Query Match 8.1%; Score 222.5; DB 2; Length 472;
Best Local Similarity 22.0%; Pred. No. 1.1e-10;
Matches 93; Conservative 79; Mismatches 152; Indels 99; Gaps 16;
QY 123 WNTVNAIQGMFVLGLPYAILHGG---YLGFLIIFAAVVCYCTKILIAAC-----LYE 172
Db 55 FNLGNAIMGSGILGLAYMAHTGVIFLALLCI--ALLSSYSHLLTTCAGIAGIRAYE 112
QY 173 E-----NEDGEVVRVDSVVAIANACAPRPTLGRVNVVAQIIELVMTCILYV---- 222
Db 113 QLGORAFGPAGKV-----VATVICHNVGAMESYLFIIKSELPVIGTFLYMDPEG 164
QY 223 --VVSNGMLNYSFPLPVSKWSIIATAVLLPCAFKLNKAV---SKESLLCTLAHFVI 277
Db 165 DWFLKGNLLI-----IIVSVLIILPLAKXHLGCLGYTSGLSLTCML--FFLV 210
QY 278 NILVIAVCL-----SRADWAEKVKFYIDVKKPPIISIGIIVFSY 317
Db 211 SVIYKFKQLGCAIGHNETAMESEALVGLPSQGLNSCEAQMFTVD--SQMSYTPINAFAP 269
QY 318 TSQIFLPSLEGNMOOSE--FHCMMWNTHIAACVLKGLFALVAYLTWADETKEVITD--N 373
Db 270 VCHPEVLPIYTELCRPSRRNQAVNVISIGMFCMTGLTATFGYLTFFYSVKAEMLHMYS 329
QY 374 LPSIRAVVNIPLVAKALLSYPLFPFAAVEVLEKSLFQEGSRAPFPACYSYDGRKLSWGL 433
Db 330 QKDPILCLVRLAVLLAVTPVPLPPIRALQQLF-----PGKAFSWPR 375
QY 434 TLRCALVWFTL--LMAIYVPHFALLMGLTSGLTGAGLCFLPLSLFHLRL-----W 482
Db 376 HVAIALILLVNVNLVCVPTIRDFGVIGTSGAPSILFILPSIFYIRIVPSEVPEPLSW 435
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QY 483 RKL 485

Db 436 PKI 438

Search completed: November 8, 2004, 18:55:54  
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:40:25 ; Search time 464 Seconds  
 (without alignments)  
 651.017 Million cell updates/sec

Title: US-09-940-919-2  
 Perfect score: 2750  
 Sequence: 1 MATLLRSKLSNVASVSNKS.....SGFVHSLEGLIAYRTNAED 525

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2750	100.0	525	1	VIAA_HUMAN	Q9H598 homo sapien
2	2731	99.3	525	1	VIAA_MACFA	Q9SKE2 macaca fasc
3	2703	98.3	525	1	VIAA_MOUSE	Q35633 mus musculus
4	2700	98.2	525	1	VIAA_RAT	Q35458 rattus norv
5	2434.5	88.5	518	2	Q6PF45	Q6PF45 xenopus lae
6	2434.5	88.5	518	2	AAH57733	AAH57733 xenopus l
7	2423.5	88.1	518	2	Q6DI16	Q6DI16 xenopus tro
8	1233.5	46.7	638	2	Q75R26	Q75R26 ciona intes
9	1283.5	46.7	638	2	BAD06308	BAD06308 ciona int
10	1081.5	39.3	549	2	Q7QH86	Q7QH86 anopheles g
11	1075	39.1	549	2	Q9V6V7	Q9V6V7 drosophila
12	858	31.2	486	1	UN47_CAEEL	UN47_CAEEL caenorhabd
13	853	31.0	164	2	Q8SP70	Q8SP70 macaca mula
14	375.5	13.7	455	2	Q7XU18	Q7XU18 oryza sativ
15	367.5	13.4	455	2	Q6YU97	Q6YU97 oryza sativ
16	367.5	13.4	455	2	BAD08181	BAD08181 oryza sat
17	346.5	12.6	526	2	Q8LFP4	Q8LFP4 oryza sativ
18	341	12.4	424	2	Q94D27	Q94D27 oryza sativ
19	334.5	12.2	550	2	Q8GYS4	Q8GYS4 arabidopsis
20	332	12.1	550	2	Q949Y8	Q949Y8 arabidopsis
21	330.5	11.7	516	2	Q9L2L5	Q9L2L5 arabidopsis
22	330.5	11.7	516	2	Q80668	Q80668 arabidopsis
23	317	11.5	543	2	Q9L2L4	Q9L2L4 arabidopsis
24	316.5	11.5	407	2	Q8H139	Q8H139 arabidopsis
25	316	11.5	425	2	Q7XQJ4	Q7XQJ4 oryza sativ
26	310	11.3	397	2	Q1XUV9	Q1XUV9 oryza sativ
27	306	11.1	449	2	Q17275	Q17275 caenorhabd
28	303	11.0	424	2	Q84Y18	Q84Y18 oryza sativ
29	302	11.0	491	2	Q7Q4M8	Q7Q4M8 anopheles g
30	301.5	11.0	478	2	Q9SR29	Q9SR29 arabidopsis
31	299.5	10.9	455	2	O45936	O45936 caenorhabd

32 299 10.9 413 2 Q8GXJ5  
 33 296.5 10.8 432 2 Q9SP09  
 34 295.5 10.7 436 2 Q9SVG0  
 35 295 10.7 422 2 Q6ESP5  
 36 295 10.7 429 2 Q9MBG9  
 37 294.5 10.7 436 2 Q8LA14  
 38 285 10.4 571 2 Q9SV32  
 39 284.5 10.3 476 2 Q9PM43  
 40 284 10.3 427 2 Q9FKV3  
 41 283.5 10.3 443 2 Q8LOU5  
 42 279.5 10.2 418 2 Q84YX7  
 43 275.5 10.0 432 2 O24406  
 44 272 9.9 426 2 Q9LFE3  
 45 268.5 9.8 481 2 Q9SR30

## ALIGNMENTS

RESULT 1  
 VIAA\_HUMAN  
 ID VIAA\_HUMAN STANDARD; PRT; 525 AA.  
 AC Q9H598; Q8N489;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vesicular inhibitory amino acid transporter (GABA and glycine  
 DE transporter) (Vesicular GABA transporter) (hVIAAT).  
 DE Name=VIAAT; Synonyms=VGAT;  
 GN Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=22027589; PubMed=12031963;  
 RX Chesser S.D., Simonson W.T., Sweet I.R., Hammerle L.P.;  
 RT "Expression of the vesicular inhibitory amino acid transporter in  
 RT pancreatic islet cells: distribution of the transporter within rat  
 RT islets.";  
 RL Diabetes 51:1763-1771 (2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC PubMed=14702039; DOI=10.1038/ng1285;  
 RX Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RX Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RX Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RX Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
 RX Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
 RX Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
 RX Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RX Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,  
 RX Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
 RX Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa K., Chiba Y.,  
 RX Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
 RX Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
 RX Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RX Imose N., Musashino K., Yuuki H., Oshima N., Sasaki N., Aotsuka S.,  
 RX Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RX Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RX Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RX Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RX Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RX Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RX Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo K., Ohmori Y.,  
 RX Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RX Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RX Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RX Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RX Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RX Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Chara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RL cDNAs.";  
 RN Nat. Genet. 36:40-45(2004).  
 [3]  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.L., Bead L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blake S.E., Bridgman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehar M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prachinham S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.,  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RN Nature 414:865-871(2001).  
 [4]  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish N.K.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.C., Gough J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RX MEDLINE=22110478; PubMed=12115694; DOI=10.1002/cne.10272;  
 RA Jellali A., Stussl-Garud C., Gaenier B., Rendon A., Sahel J.-A.,  
 RA Dreyfus H., Picaut S.;  
 RT "Cellular localization of the vesicular inhibitory amino acid  
 RL transporter in the mouse and human retina.";  
 CC J. Comp. Neurol. 449:176-87(2002).  
 -!- FUNCTION: Involved in the uptake of GABA and glycine into the  
 CC synaptic vesicles.  
 -!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular  
 CC membrane vesicles (By similarity).  
 -!- TISSUE SPECIFICITY: Retina. Expressed throughout the horizontal  
 CC cells or more specifically at the terminals.  
 -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family

CC II.  
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 CC -----  
 DR EMBL; AY044836; AAK38782.1; -;  
 DR EMBL; AK055051; BAB70846.1; -;  
 DR EMBL; AL133519; CAC15529.2; -;  
 DR EMBL; BC036458; AAH36458.2; ALT\_INIT.  
 DR EMBL; BC035582; AAH53582.1; -;  
 DR Genes; HGNC:15800; VIANT.  
 DR InterPro; IPR002422; AA/rel\_permease2.  
 DR Pfam; PF01490; Aa\_trans; 1.  
 KW Glycoprotein; Neurotransmitter transport; Transmembrane; Transport.  
 FT DOMAIN 1 133 Cytoplasmic (Potential).  
 FT DOMAIN 134 154 Vesicular lumen (Potential).  
 FT DOMAIN 155 204 Potential.  
 FT DOMAIN 205 225 Potential.  
 FT DOMAIN 226 242 Cytoplasmic (Potential).  
 FT DOMAIN 243 263 Potential.  
 FT DOMAIN 264 265 Vesicular lumen (Potential).  
 FT DOMAIN 266 286 Potential.  
 FT DOMAIN 287 305 Cytoplasmic (Potential).  
 FT DOMAIN 306 326 Potential.  
 FT DOMAIN 327 341 Vesicular lumen (Potential).  
 FT DOMAIN 342 362 Potential.  
 FT DOMAIN 363 383 Cytoplasmic (Potential).  
 FT DOMAIN 384 404 Potential.  
 FT DOMAIN 405 438 Vesicular lumen (Potential).  
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 FT DOMAIN 483 489 Vesicular lumen (Potential).  
 FT DOMAIN 490 510 Potential.  
 FT DOMAIN 511 525 Cytoplasmic (Potential).  
 FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 261 261 K -> R (in Ref. 4; AAK36458).  
 SQ SEQUENCE 525 AA; 57415 MW; C3C4B0786B8D745 CRC64;  
 Query Match 100.0%; Score 2750; DB 1; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-195;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MATLRSKLSNVATSVSNKSKQAMSGMFMFGQAATDEAVGFAHCDLDFEHRQGLQM 60  
 DB 1 MATLRSKLSNVATSVSNKSKQAMSGMFMFGQAATDEAVGFAHCDLDFEHRQGLQM 60  
 QY 61 DILKAEGPSGDEGAEPVSGDIHYQKSGAPPPSGSKDQVGGGFGGCHKPITAW 120  
 DB 61 DILKAEGPSGDEGAEPVSGDIHYQKSGAPPPSGSKDQVGGGFGGCHKPITAW 120  
 QY 121 AGNVTVAIQGMFVLGLPYAILHGGVGLFLIIFAAVWCYTGKILIAEENDEGEV 180  
 DB 121 AGNVTVAIQGMFVLGLPYAILHGGVGLFLIIFAAVWCYTGKILIAEENDEGEV 180  
 QY 181 RVRDSYVAIANACCAFRPFLTGGVNVVAQIIELVMTCTILYVNVGNLMYNSFPGLPVSQ 240  
 DB 181 RVRDSYVAIANACCAFRPFLTGGVNVVAQIIELVMTCTILYVNVGNLMYNSFPGLPVSQ 240  
 QY 241 KWSIIATAVLLPCAFILKLVKAVKFSLLCTLAHFVNLIVAYCLSRARDWAKVFPY 300  
 DB 241 KWSIIATAVLLPCAFILKLVKAVKFSLLCTLAHFVNLIVAYCLSRARDWAKVFPY 300  
 QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNWQSPSEPHCMNMWTHIAACVKGFLPVA 360  
 DB 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNWQSPSEPHCMNMWTHIAACVKGFLPVA 360  
 QY 361 TWADETKEVITDNLPGSIRAVNVNIFLVAKALLSYLPFFFAVEVLEKSLFQEGSRA 420

Db 361 TWADETEKVTNLPGRSIRAVVNIPLVAKALLSYLPFFFAVEVLEKSLFQSGRAFFPA 420  
 QY 421 CYSGDGRKSWGLRLCALVFTLLMAIYVPHFALLMGLTSGTGAAGLCLLPSLFHLRL 480  
 Db 421 CYSGDGRKSWGLRLCALVFTLLMAIYVPHFALLMGLTSGTGAAGLCLLPSLFHLRL 480  
 QY 481 LWRKLLHWHQVFDVAIFVIGGICSVSGFVHSLGLELIAYRTNAED 525  
 Db 481 LWRKLLHWHQVFDVAIFVIGGICSVSGFVHSLGLELIAYRTNAED 525

## RESULT 2

VIAA\_MACFA STANDARD; PRT; 525 AA.  
 AC Q95KE2;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Vesicular inhibitory amino acid transporter (GABA and glycine transporter) (Vesicular GABA transporter) (QCCE-21149).  
 GN Name=VIAAT; Synonyms=VGAT;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Involved in the uptake of GABA and glycine into the synaptic vesicles (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular membrane vesicles (By similarity).  
 CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family II.  
 CC  
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 CC  
 CC EMBL; AB062931; BAB60726.1; -;  
 DR InterPro; IPR002422; AA/rel\_permease2.  
 DR Pfam; PF01490; Aa trans; 1.  
 KW Glycoprotein; Neurotransmitter transporter; Transmembrane; Transport.  
 FT DOMAIN 1 133 Cytoplasmic (Potential).  
 FT TRANSMEM 134 154 Potential.  
 FT DOMAIN 155 204 Vesicular lumen (Potential).  
 FT TRANSMEM 205 225 Potential.  
 FT DOMAIN 226 242 Cytoplasmic (Potential).  
 FT TRANSMEM 243 263 Potential.  
 FT DOMAIN 264 265 Vesicular lumen (Potential).  
 FT TRANSMEM 266 286 Potential.  
 FT DOMAIN 287 305 Cytoplasmic (Potential).  
 FT TRANSMEM 306 326 Potential.  
 FT DOMAIN 327 341 Vesicular lumen (Potential).  
 FT TRANSMEM 342 362 Potential.  
 FT DOMAIN 363 383 Cytoplasmic (Potential).  
 FT TRANSMEM 384 404 Potential.  
 FT DOMAIN 405 438 Vesicular lumen (Potential).  
 FT TRANSMEM 439 459 Potential.  
 FT DOMAIN 460 461 Cytoplasmic (Potential).  
 FT TRANSMEM 462 482 Potential.  
 FT DOMAIN 483 Vesicular lumen (Potential).

FT TRANSMEM 490 510 Potential.  
 FT DOMAIN 511 525 Cytoplasmic (Potential).  
 FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 525 AA; 57393 MW; 2CF17504CB2FDC9 CRC64;  
 Query Match 99.3%; Score 2731; DB 1; Length 525;  
 Best Local Similarity 99.2%; Pred. No. 6.9e-194;  
 Matches 521; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MATLLRSKLSNVATSVSNKSQAQKSGMFMARMGFQAATDEEAVGFAHCDLDFEHRQGLQM 60  
 Db 1 MATLLRSKLSNVATSVSNKSQAQKSGMFMARMGFQAATDEEAVGFAHCDLDFEHRQGLQM 60  
 QY 61 DILKAEGEPCGDEGAEPVEGDIHYQRSGGAPLPSPGSKDQVGGGEGFGCHDKPKITAVE 120  
 Db 61 DILKAEGEPCGDEGAEPVEGDIHYQRSGGAPLPSPGSKDQVGGGEGFGCHDKPKITAVE 120  
 QY 121 AGNNVTNAIQGMFVLGFLPYAILHGGVGLFLIIFAAVVCCYTGKILIACLYEENEDGEVV 180  
 Db 121 AGNNVTNAIQGMFVLGFLPYAILHGGVGLFLIIFAAVVCCYTGKILIACLYEENEDGEVV 180  
 QY 181 RVDSYVAIANACCAPRPPTLGGRVNVNAQIIELVNTCILYVVSGLNLMYNSFPGLPVSQ 240  
 Db 181 RVDSYVAIANACCAPRPPTLGGRVNVNAQIIELVNTCILYVVSGLNLMYNSFPGLPVSQ 240  
 QY 241 KWSIIATATVLLPCAFLLKNAKSKFSLCLTAHFVINILVIATYCLSRARDWAEKVKFY 300  
 Db 241 KWSIIATATVLLPCAFLLKNAKSKFSLCLTAHFVINILVIATYCLSRARDWAEKVKFY 300  
 QY 301 IDVKFPFISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMNMTHTAACVLKGLFALVAYL 360  
 Db 301 IDVKFPFISIGIIVFSYTSQIFLPSLEGNMQQPSFHCMMNMTHTAACVLKGLFALVAYL 360  
 QY 361 TWADETEKVTNLPGRSIRAVVNIPLVAKALLSYLPFFFAVEVLEKSLFQSGRAFFPA 420  
 Db 361 TWADETEKVTNLPGRSIRAVVNIPLVAKALLSYLPFFFAVEVLEKSLFQSGRAFFPA 420  
 QY 421 CYSGDGRKSWGLRLCALVFTLLMAIYVPHFALLMGLTSGTGAAGLCLLPSLFHLRL 480  
 Db 421 CYSGDGRKSWGLRLCALVFTLLMAIYVPHFALLMGLTSGTGAAGLCLLPSLFHLRL 480  
 QY 481 LWRKLLHWHQVFDVAIFVIGGICSVSGFVHSLGLELIAYRTNAED 525  
 Db 481 LWRKLLHWHQVFDVAIFVIGGICSVSGFVHSLGLELIAYRTNAED 525  
 RESULT 3  
 VIAA\_MOUSE STANDARD; PRT; 525 AA.  
 AC O35633;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vesicular inhibitory amino acid transporter (GABA and glycine transporter) (Vesicular GABA transporter) (mVIAAT) (mVGAT).  
 DE Name=VIAAT; Synonyms=Vgat;  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=98055669; PubMed=9395291;  
 RA Sagne C., Bl Westikawy S., Isambert M.-F., Hamon M., Henry J.-P., Giros B.P., Gasnier B.;  
 RT "Cloning of a functional vesicular GABA and glycine transporter by screening of genome databases."  
 RL FEBS Lett. 417:177-183(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=22461323; PubMed=12573541;  
 RA Ebihara S., Obata K., Yanagawa Y.;

"Mouse vesicular GABA transporter gene: genomic organization, transcriptional regulation and chromosomal localization.",  
Brain Res. Mol. Brain Res. 110:126-139(2003).  
(3)  
SEQUENCE FROM N.A. (ISOFORM 1).  
STRAIN=C57BL/6; TISSUE=Brain;  
MEDLINE=22389257; PubMed=12417932; DOI=10.1073/pnas.242603899;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,  
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.",  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
(4)  
TISSUE SPECIFICITY  
MEDLINE=22110478; PubMed=12115694; DOI=10.1002/cne.10272;  
Jellali A., Stussi-Garand C., Gasnier B., Rendon A., Sahel J.-A.,  
Dreyfus H., Picaut S.;  
"Cellular localization of the vesicular inhibitory amino acid  
transporter in the mouse and human retina.",  
J. Comp. Neurol. 449:76-87(2002).  
-!- FUNCTION: Involved in the uptake of GABA and glycine into the  
synaptic vesicles.  
-!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular  
membrane vesicles (By similarity).  
-!- ALTERNATIVE PRODUCTS  
Event=Alternative splicing; Named isoforms=2;  
Name1: Synonyms=b;  
IsoId=035633-1; Sequence=Displayed;  
Name2; Synonyms=a;  
IsoId=035633-2; Sequence=VSP\_007063;  
-!- TISSUE SPECIFICITY: Brain and retina. Localized in horizontal cell  
tips at both rod and cone terminals.  
-!- SIMILARITY: Belongs to the amino acid/polyamine transporter family  
II.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AB080232; BAC44888.1; -;  
EMBL; AB080232; BAC44889.1; -;  
EMBL; AJ001598; CAA04864.1; -;  
EMBL; BC052020; AAH52020.1; -;  
EMBL; MGI:1194488; Viaat.  
GO; GO:0005887; C: integral to plasma membrane; IC.  
GO; GO:0005331; P: gamma-aminobutyric acid transporter activity; IDA.  
GO; GO:0015187; P: glycine transporter activity; IDA.  
GO; GO:0015816; P: glycine transport; IDA.  
InterPro; IPR002422; AA/rel\_permease2.  
Pfam; PF01490; Aa trans; 1.  
KW Alternative splicing; Glycoprotein; Neurotransmitter transport;  
Transmembrane; Transport.  
DOMAIN 1 133 Cytoplasmic (Potential).  
FT 134 154 Potential.

FT	DOMAIN	155	204	Vesicular lumen (Potential):
FT <td>TRANSMEM</td> <td>205</td> <td>245</td> <td>Potential.</td>	TRANSMEM	205	245	Potential.
FT <td>TRANSMEM</td> <td>226</td> <td>242</td> <td>Cytoplasmic (Potential).</td>	TRANSMEM	226	242	Cytoplasmic (Potential).
FT <td>TRANSMEM</td> <td>243</td> <td>263</td> <td>Potential.</td>	TRANSMEM	243	263	Potential.
FT <td>TRANSMEM</td> <td>264</td> <td>265</td> <td>Vesicular lumen (Potential).</td>	TRANSMEM	264	265	Vesicular lumen (Potential).
FT <td>TRANSMEM</td> <td>287</td> <td>305</td> <td>Potential.</td>	TRANSMEM	287	305	Potential.
FT <td>TRANSMEM</td> <td>306</td> <td>326</td> <td>Cytoplasmic (Potential).</td>	TRANSMEM	306	326	Cytoplasmic (Potential).
FT <td>TRANSMEM</td> <td>327</td> <td>341</td> <td>Potential.</td>	TRANSMEM	327	341	Potential.
FT <td>TRANSMEM</td> <td>342</td> <td>362</td> <td>Vesicular lumen (Potential).</td>	TRANSMEM	342	362	Vesicular lumen (Potential).
FT <td>TRANSMEM</td> <td>363</td> <td>384</td> <td>Potential.</td>	TRANSMEM	363	384	Potential.
FT <td>TRANSMEM</td> <td>385</td> <td>405</td> <td>Cytoplasmic (Potential).</td>	TRANSMEM	385	405	Cytoplasmic (Potential).
FT <td>TRANSMEM</td> <td>406</td> <td>438</td> <td>Vesicular lumen (Potential).</td>	TRANSMEM	406	438	Vesicular lumen (Potential).
FT <td>TRANSMEM</td> <td>439</td> <td>459</td> <td>Potential.</td>	TRANSMEM	439	459	Potential.
FT <td>TRANSMEM</td> <td>460</td> <td>461</td> <td>Cytoplasmic (Potential).</td>	TRANSMEM	460	461	Cytoplasmic (Potential).
FT <td>TRANSMEM</td> <td>462</td> <td>482</td> <td>Potential.</td>	TRANSMEM	462	482	Potential.
FT <td>TRANSMEM</td> <td>483</td> <td>489</td> <td>Vesicular lumen (Potential).</td>	TRANSMEM	483	489	Vesicular lumen (Potential).
FT <td>TRANSMEM</td> <td>490</td> <td>510</td> <td>Potential.</td>	TRANSMEM	490	510	Potential.
FT <td>TRANSMEM</td> <td>511</td> <td>525</td> <td>Cytoplasmic (Potential).</td>	TRANSMEM	511	525	Cytoplasmic (Potential).
FT <td>CARBOHYD</td> <td>341</td> <td>341</td> <td>N-linked (GlcNAc. .) (Potential).</td>	CARBOHYD	341	341	N-linked (GlcNAc. .) (Potential).
FT <td>VARSPLIC</td> <td>515</td> <td>525</td> <td>LIEAYRTNAED -&gt; KFAGLET (in isoform 2). /FTId=VSP_007063.</td>	VARSPLIC	515	525	LIEAYRTNAED -> KFAGLET (in isoform 2). /FTId=VSP_007063.
FT <td>CONFLICT</td> <td>432</td> <td>432</td> <td>G -&gt; E (in Ref. 1).</td>	CONFLICT	432	432	G -> E (in Ref. 1).
SQ <td>SEQUENCE</td> <td>525 AA;</td> <td>57381 MW;</td> <td>EBD63E01A4B54C07 CRC64;</td>	SEQUENCE	525 AA;	57381 MW;	EBD63E01A4B54C07 CRC64;

  

Query Match	Score	2703;	DB 1;	Length	525;
Best Local Similarity	98.3%;				
Matches	518;	Conservative	4;	Mismatches	2;
				Indels	2;
				Gaps	2;

  

QY	1	MATLRSKLSNVATSVSNKSKQAKSGMFARMFOAATDEEAVGFAHCDLDFEHRQGLQ	60
DB <td>1 <td>MATLRSKLTNTVATSVSNKSKQAKSGMFARMFOAATDEEAVGFAHCDLDFEHRQGLQ <td>60</td> </td></td>	1 <td>MATLRSKLTNTVATSVSNKSKQAKSGMFARMFOAATDEEAVGFAHCDLDFEHRQGLQ <td>60</td> </td>	MATLRSKLTNTVATSVSNKSKQAKSGMFARMFOAATDEEAVGFAHCDLDFEHRQGLQ <td>60</td>	60
QY <td>61 <td>DILKAEPEPCGDEGAEPVEGDHYQSGAPLPSPSSKQD-VGGGEFGHDKPKITAW <td>119</td> </td></td>	61 <td>DILKAEPEPCGDEGAEPVEGDHYQSGAPLPSPSSKQD-VGGGEFGHDKPKITAW <td>119</td> </td>	DILKAEPEPCGDEGAEPVEGDHYQSGAPLPSPSSKQD-VGGGEFGHDKPKITAW <td>119</td>	119
DB <td>61 <td>DILKSEGPCGDEGAEPVEGDHYQSGAPLPSPSSKQDQAVGAGGFGHDKPKITAW <td>119</td> </td></td>	61 <td>DILKSEGPCGDEGAEPVEGDHYQSGAPLPSPSSKQDQAVGAGGFGHDKPKITAW <td>119</td> </td>	DILKSEGPCGDEGAEPVEGDHYQSGAPLPSPSSKQDQAVGAGGFGHDKPKITAW <td>119</td>	119
QY <td>120 <td>EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td> </td></td>	120 <td>EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td> </td>	EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td>	179
DB <td>120 <td>EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td> </td></td>	120 <td>EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td> </td>	EAGNVNTNAIQGMFVLGLPYAILHGGVGLFLITFAAVCCYTKILLIACLYENEDGEV <td>179</td>	179
QY <td>180 <td>VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td> </td></td>	180 <td>VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td> </td>	VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td>	239
DB <td>180 <td>VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td> </td></td>	180 <td>VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td> </td>	VRVRSYVAIANACCAPRFTLGGRVNVNAQIIELVMTCLYVVVSGNLMYNSPGLPVS <td>239</td>	239
QY <td>240 <td>QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td> </td></td>	240 <td>QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td> </td>	QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td>	299
DB <td>240 <td>QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td> </td></td>	240 <td>QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td> </td>	QKWSIIATAVLLCAFLKNIKAVSKSLCTLAHFVNILVIAYCLSRARDMAWEKVF <td>299</td>	299
QY <td>300 <td>YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td> </td></td>	300 <td>YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td> </td>	YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td>	359
DB <td>300 <td>YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td> </td></td>	300 <td>YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td> </td>	YIDVKKFPISGIIVFSYTSQIFLPSLEGNMQQSEFHCMMNTHIAACVLKGLFALVAY <td>359</td>	359
QY <td>360 <td>LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td> </td></td>	360 <td>LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td> </td>	LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td>	419
DB <td>360 <td>LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td> </td></td>	360 <td>LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td> </td>	LTWADETKEVITDNLPGSIRAVNIFLVAKALLSYPLFPFAAIVELEKSLFOESRAFPF <td>419</td>	419
QY <td>420 <td>ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td> </td></td>	420 <td>ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td> </td>	ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td>	479
DB <td>420 <td>ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td> </td></td>	420 <td>ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td> </td>	ACYSGDGLKSWGLTLRCALVVFLLMAIYVPHFALLMGLTSGTLAGLCLFLLPSFLHR <td>479</td>	479
QY <td>480 <td>LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td> </td></td>	480 <td>LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td> </td>	LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td>	525
DB <td>480 <td>LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td> </td></td>	480 <td>LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td> </td>	LLWRKLLHQVFFDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED <td>525</td>	525

  

RESULT 4	VIAA_RAT	STANDARD;	PRT;	525 AA.
ID	VIAA_RAT			
AC	O35458;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			



DE Vesicular inhibitory amino acid transporter (GABA and glycine  
 DE transporter) (Vesicular GABA transporter) (rGAT).  
 GN Name-Viaat; Synonyms=Vgat;  
 OS Rattus norvegicus (Rat);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98007977; PubMed=9349821;  
 RA McIntire S.L., Reimer R.J., Schuke K., Edwards R.H., Jorgensen E.M.;  
 RT "Identification and characterization of the vesicular GABA  
 RT transporter.";  
 RL Nature 389:870-876 (1997).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC TISSUE=Brain.  
 RX MEDLINE=22027589; PubMed=12031963;  
 RA Chessler S.D., Simonsen W.T., Sweet I.R., Hammerle L.P.;  
 RT "Expression of the vesicular inhibitory amino acid transporter in  
 RT pancreatic islet cells: distribution of the transporter within rat  
 RT islets.";  
 RL Diabetes 51:1763-1771 (2002).  
 CC -!- FUNCTION: Involved in the uptake of GABA and glycine into the  
 CC synaptic vesicles.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular  
 CC membrane vesicles.  
 CC -!- TISSUE SPECIFICITY: Brain. Expressed at high levels within the  
 CC neocortex, hippocampus, cerebellum, striatum, septal nuclei and  
 CC the reticular nucleus of the thalamus. Also expressed in islets  
 CC where it is more abundant in the peripheral/mantle region.  
 CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family  
 CC II.

-----  
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 CC -----

DR EMBL; AF030253; AAB82950.1; -;  
 DR RGD; 621402; Viaat  
 DR InterPro; IPR002422; AA/rel\_permease2.  
 DR Pfam; PF01490; Aa\_trans; 1.  
 KW Glycoprotein; Neurotransmitter transport; Transmembrane; Transport.  
 FT DOMAIN 1 133  
 FT 134 154 Cytoplasmic (Potential).  
 FT 155 204 Potential.  
 FT 205 225 Vesicular lumen (Potential).  
 FT 226 242 Potential.  
 FT 243 263 Cytoplasmic (Potential).  
 FT 264 286 Vesicular lumen (Potential).  
 FT 287 305 Potential.  
 FT 306 326 Cytoplasmic (Potential).  
 FT 327 341 Potential.  
 FT 342 362 Vesicular lumen (Potential).  
 FT 363 383 Potential.  
 FT 384 404 Cytoplasmic (Potential).  
 FT 405 438 Vesicular lumen (Potential).  
 FT 439 459 Potential.  
 FT 460 481 Cytoplasmic (Potential).  
 FT 482 499 Potential.  
 FT 500 510 Vesicular lumen (Potential).  
 FT 511 525 Potential.  
 FT 526 540 Cytoplasmic (Potential).  
 FT CARBOHYD 341 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 525 AA; 57407 MW; 33C5E8D31B7BD510 CRC64;

Query Match

98.2%; Score 2700; DB 1; Length 525;

Best Local Similarity 98.5%; Pred. No. 1.4e-191;  
 Matches 518; Conservative 3; Mismatches 3; Indels 2; Gaps 2;  
 QY 1 MATLLSKLSNVATSVSNKSKQKMSQFARMGFOAATDEAVGFAHCDLDFEHROGLQ 60  
 DB 1 MATLLSKLNTVATSVSNKSKQKMSQFARMGFOAATDEAVGFAHCDLDFEHROGLQ 60  
 QY 61 DILKARGPCGDEGAEAPVEGDHYHORGSGAPLPPSGSKDQ-VGGGEGFGGHDKPKITAW 119  
 DB 61 DILKSGEGPCGDEGAEAPVEGDHYHORG-GAPLPPSGSKDQAVGAGGEGFGHDKPKITAW 119  
 QY 120 EAGWNTNAIQGMFVLGLPYAILHGGYGLFLIIIPAAVCCYTKGLIACLYEENEDGEV 179  
 DB 120 EAGWNTNAIQGMFVLGLPYAILHGGYGLFLIIIPAAVCCYTKGLIACLYEENEDGEV 179  
 QY 180 VVRVDSYVAIANACCAPRPTLGGRVVNVAAQIIELVMTCILYVVSNGNLMYNSFPGLPVS 239  
 DB 180 VVRVDSYVAIANACCAPRPTLGGRVVNVAAQIIELVMTCILYVVSNGNLMYNSFPGLPVS 239  
 QY 240 QKSWSIATAVLLPCCAFKLVKAVSKFSLCTLAHFVNILVIAIYCLSRADWAEKVKF 299  
 DB 240 QKSWSIATAVLLPCCAFKLVKAVSKFSLCTLAHFVNILVIAIYCLSRADWAEKVKF 299  
 QY 300 YIDVKFPIISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNTHIAACVLKGLPALVAY 359  
 DB 300 YIDVKFPIISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNTHIAACVLKGLPALVAY 359  
 QY 360 LTWADTKETITDNLPGSIRAVVNIFLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFP 419  
 DB 360 LTWADTKETITDNLPGSIRAVVNIFLVAKALLSYPLPFAAVEVLEKSLFOEGSRAPFP 419  
 QY 420 ACYSGDGRKSLGTLRCALVWFTLLMALIYVPHFALLMGLTGLTGAICFLPLSLFHLR 479  
 DB 420 ACYSGDGRKSLGTLRCALVWFTLLMALIYVPHFALLMGLTGLTGAICFLPLSLFHLR 479  
 QY 480 LLWRKLLMHQVFPDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525  
 DB 480 LLWRKLLMHQVFPDVAIFVIGGICSVSGFVHSLGLEIAYRTNAED 525

RESULT 5  
 Q6PPF45 / PRELIMINARY; PRT; 518 AA.  
 ID Q6PPF45  
 AC Q6PPF45;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE MG68938 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX Klein S., Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057733; AAH57733.1; -  
DR InterPro; IPR002422; AA/rel\_permease2.  
DR Pfam; PF01490; Aa trans; 1.  
SQ SEQUENCE 518 AA; 57190 MW; 0DE19ED16BD84C0D CRC64;  
  
Query Match 88.5%; Score 2434.5; DB 2; Length 518;  
Best Local Similarity 89.5%; Pred. No. 6.3e-172;  
Matches 470; Conservative 19; Mismatches 29; Indels 7; Gaps 4;  
  
QY 1 MATLRSKLSNVATSVSNKSOAKSGMFARMGFOAATDEBAVGFHACDDLDLDFHROGLQ 60  
Db 1 MATLRSKLSNVATSVSNKSOAKSGMFARMGFOAATDEBAVGFHACDDLDLDFHROGLQ 60  
  
QY 61 DILKAGEPCDGEAGAEVVEGDIIHQSGGAPLPSPSGKQVGGGGFGHDKPKITAW 120  
Db 61 DILKTE-VPTGD-APPEGDIIHQYR-DGTGLPSPASKDE-GLCSELSSEKPKITAW 113  
  
QY 121 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 180  
Db 121 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 180  
  
QY 144 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 173  
Db 144 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 173  
  
QY 181 RVDSYVAIANACAPRPTLGGRVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQ 240  
Db 174 RVDSYVDIANACAPRPTLGGRVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQ 233  
  
QY 241 KWSIATATVLLPCAFNLKAVSKFSLCTLAHFVNILVIAVCLSPARDWAKVKFY 300  
Db 234 KWSIMATATVLLPCAFNLKAVSKFSLCTLAHFVNILVIAVCLSPARDWAKVKFY 293  
  
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTTHIAACVLKGLFALVAYL 360  
Db 294 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQSPREFHCMMNWTTHIAACVLKGLFALVAYL 353  
  
QY 361 TWADETKEVITDNLPGSTRVAVNVLVAKALLSYPLPFAAVEVLEKSLFQEGSRAPFA 420  
Db 354 TWADETKEVITDNLPGSTRVAVNVLVSKALLSYPLPFAAVEVLEKSLFQEGSRAPFA 413  
  
QY 421 CYSGDGLKSLGTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLPHRL 480  
Db 414 CYSGDGLKSLGTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLPHRL 473  
  
QY 481 LWRKLLHQVFFDVAIFVIGSICVSFGVHSLEGLIEAYNTNED 525  
Db 474 MWRQLLHQVFFDVAIFVIGSICVSFGVHSLEGLIEAYNTNED 518  
  
RESULT 6  
AAH57733  
ID AAH57733 PRELIMINARY; PRT; 518 AA.  
AC AAH57733;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE MGC68938 protein.  
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8395;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057733; AAH57733.1; -  
SQ SEQUENCE 518 AA; 57190 MW; 0DE19ED16BD84C0D CRC64;  
  
Query Match 88.5%; Score 2434.5; DB 2; Length 518;  
Best Local Similarity 89.5%; Pred. No. 6.3e-172;  
Matches 470; Conservative 19; Mismatches 29; Indels 7; Gaps 4;  
  
QY 1 MATLRSKLSNVATSVSNKSOAKSGMFARMGFOAATDEBAVGFHACDDLDLDFHROGLQ 60  
Db 1 MATLRSKLSNVATSVSNKSOAKSGMFARMGFOAATDEBAVGFHACDDLDLDFHROGLQ 60  
  
QY 61 DILKAGEPCDGEAGAEVVEGDIIHQSGGAPLPSPSGKQVGGGGFGHDKPKITAW 120  
Db 61 DILKTE-VPTGD-APPEGDIIHQYR-DGTGLPSPASKDE-GLCSELSSEKPKITAW 113  
  
QY 121 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 180  
Db 121 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 180  
  
QY 144 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 173  
Db 144 AGWNVNVAIQGMFVLGLPYAILHGYLGLFLIIFAAVVCCVTGKILIACTEENEDGEV 173  
  
QY 181 RVDSYVAIANACAPRPTLGGRVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQ 240  
Db 174 RVDSYVDIANACAPRPTLGGRVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQ 233  
  
QY 241 KWSIATATVLLPCAFNLKAVSKFSLCTLAHFVNILVIAVCLSPARDWAKVKFY 300  
Db 234 KWSIMATATVLLPCAFNLKAVSKFSLCTLAHFVNILVIAVCLSPARDWAKVKFY 293  
  
QY 301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSEFHCMMNWTTHIAACVLKGLFALVAYL 360  
Db 294 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQSPREFHCMMNWTTHIAACVLKGLFALVAYL 353  
  
QY 361 TWADETKEVITDNLPGSTRVAVNVLVAKALLSYPLPFAAVEVLEKSLFQEGSRAPFA 420  
Db 354 TWADETKEVITDNLPGSTRVAVNVLVSKALLSYPLPFAAVEVLEKSLFQEGSRAPFA 413  
  
QY 421 CYSGDGLKSLGTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLPHRL 480  
Db 414 CYSGDGLKSLGTLRCALVFTLLMAIYVPHFALLMGLTGSAGLCLFLLPSLPHRL 473  
  
QY 481 LWRKLLHQVFFDVAIFVIGSICVSFGVHSLEGLIEAYNTNED 525  
Db 474 MWRQLLHQVFFDVAIFVIGSICVSFGVHSLEGLIEAYNTNED 518  
  
RESULT 6  
AAH57733  
ID AAH57733 PRELIMINARY; PRT; 518 AA.  
AC AAH57733;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE MGC68938 protein.  
OS Xenopus laevis (African clawed frog).

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QY 361 TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPPPA 420
DB 354 TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPPPA 413
QY 421 CYSGDGRKSLGLTRCALVVFLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLFLHL 480
DB 414 CYGGDRKSLGLTRCALVVFLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLFLHL 473
QY 481 LWRKLLMHQVFFDVAIFVIGGICSVGFVHSLGLEIAYRTNAED 525
DB 474 MWRLQLMHQVFFDVSIFVIGSICSVGFVHSLGLEIAYRTNAED 518

RESULT 7
Q6DIV6 PRELIMINARY; PRT; 518 AA.
AC Q6DIV6;
DT 01-OCT-2004 (T-EMBLrel. 28, Created)
DT 01-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075429; AAH75429.1;
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57155 NW; 1B0B04020851C78B CRC64;

Query Match 88.1%; Score 2422.5; DB 2; Length 518;
Best Local Similarity 89.3%; Pred. No. 4.9e-171;
Matches 469; Conservative 16; Mismatches 33; Indels 7; Gaps 4;

QY 1 MATLRSKLSNVATSVSNKSKQAKSGMFARMGFOAATDEEAVGFAHCDLDFEHRQGLQM 60
DB 1 MATLRSKLSNVATSVSNKSKQAKSGMFARMGFOAATDEEALGFAHCDLDMEHRQGLQM 60
QY 61 DILKAEPCGDEGAEPVEGDHIVORGSCAPLPSGSKDQVGGGEGGCHKPKITAW 120
DB 61 DILKTE-VPSGPTA-----EGDSHYQRDGTGP-PSSAKDB-GLCSELSYSGKPKITAW 113
QY 121 AGNVTNATQGMFVLGFLPYAILHGGVGLFLIFAAVCCYTGKILIAACLYEENDEGT 180

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DB 114 AGNVTNATQGMFVLGFLPYAILHGGVGLFLIFAAVCCYTGKILIAACLYEENDEGT 173
QY 181 RVDSYVAIANACCAAPRFTLGGRVVNVAQIIELVMTCTLYVYVSGNLMYNFPGLPVSQ 240
DB 174 RVDSYVDIANACCAAPRFTLGGRVVNVAQIIELVMTCTLYVYVSGNLMYNFPGLPVSQ 233
QY 241 KWSIIATATAVLPCAFELKNLKAVSKESLCTLAHFVINTLVAYCISLRARDNAWEKVKFY 300
DB 234 KWSIIATATAVLPCAFELKNLKAVSKESLCTLAHFVINTLVAYCISLRARDNAWEKVKFY 293
QY 301 IDVKKEPISIGIIVFSYTSQIFLPSLEGNMQPSPFHCMMNMWTHIAACVKGILFALVAYL 360
DB 294 IDVKKEPISIGIIVFSYTSQIFLPSLEGNMQSPKPFHCMMNMWTHIAACVKGILFALVAYL 353
QY 361 TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPPPA 420
DB 354 TWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAPPPA 413
QY 421 CYSGDGRKSLGLTRCALVVFLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLFLHL 480
DB 414 CYGGDRKSLGLTRCALVVFLLMAIYVPHFALLMGLTGLTGAGLCFLPLPSLFLHL 473
QY 481 LWRKLLMHQVFFDVAIFVIGGICSVGFVHSLGLEIAYRTNAED 525
DB 474 LWRKLLMHQVFFDVSIFVIGSICSVGFVHSLGLEIAYRTNAED 518

RESULT 8
Q7SRZ6 PRELIMINARY; PRT; 638 AA.
AC Q7SRZ6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Vesicular GABA transporter.
GN Names=Ci-wGAT;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=15170699;
RA Yoshida R., Sakurai S., Horie T., Kawakami I., Tsuda M., Kusakabe T.,
RT "Identification of neuron-specific promoters in Ciona intestinalis.";
RL Genesis 39:130-140 (2004).
DR EMBL; AB158401; BAD06308.1;
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa_Ctrans; 1.
SQ SEQUENCE 638 AA; 69532 MW; 707DC701FB409FDA CRC64;

Query Match 46.7%; Score 1283.5; DB 2; Length 638;
Best Local Similarity 44.2%; Pred. No. 1.5e-86;
Matches 244; Conservative 88; Mismatches 117; Indels 103; Gaps 6;

QY 37 TDEAVGFAHCDLDFEHRQGLQMDILKAEPCGDEGAEPVEGDI-HYQSGSAPLPP 95
DB 18 TSEKFSFAKSDQP-----HPSGSGCGDGTATPSSNSVSHPERST----- 59
QY 96 SGSKDQVGGGEGGCHKPKITAEAGNVNVAIQGMFVLGFLPYAILHGGVGLFLIF 155
DB 60 -----SGVEKPTITADAGNVNVAIQGMFVLGFLPYAVLHGGVGLFLIIVT 106
QY 156 AVCCYTGKILIAACLYEENDEGVVRVRSYVAIANACCAAPRFTLGGRVVNVAQIIELV 215
DB 107 AVCCYTGKILIDCLVETSPSGERLVRVSTYVDLAACWGHK---LGGVLVNAQAQIELL 163
QY 216 MTCILYVYVSGNLMYNFPGLPVSOXSWSIATATAVLPCAFELKNLKAVSKESLCTLAHF 275
DB 164 MTCVLYVYVSGNLMTNSFPHGPIREAGNSVLACLVLPCTFLRHRAVRFSGWCSVAQI 223
QY 276 VINILVIAYCISLRARDNAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQPSE 335

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Db 224 VVLGITIVYCIKINTWAWSEITISVDMKQFVPSIGVIVFVSQIPLPSLESGMENRGD 283
QY 336 FHCMMNTHIAACVLKGLPALVAVLTWADETKEVITDNLPGSIRAVVNIPLVAKALLSYP 395
Db 284 FRSLMSVSYASCVTKASFALICFLTWSKOTDVTDLNPTLRAMINVLVLLVALLSYP 343
QY 396 LPFFAAVEVLEKSLF----- 410
Db 344 LPYQAIEVMEQTMFTGATGGWSLFGTKRHAYGFTDDTEPIVQSTSFNTDAPSSPST 403
QY 411 -----QEG-----SRAFFPACVSGDGLKSWGLTRCALVFTLLMA 447
Db 404 TNSDGLDSDKSTTKRNVILTLEDNTKQSSCSPSCYSATGDLQVWALVLRAGLVLTLLMG 463
QY 448 IYVPHFALLMGLTSLTGAGLCFLPLSLFHLRLKLLMHQVFFDVAIFVIGGICSVSG 507
Db 464 VIPHPHALLMGLTSLTGSLAFPLPCAFHLQIKWREMKWREIGLDVFIISGTVCGITG 523
QY 508 FVHSLGLEIAY 519
Db 524 IYFSIQGLYEVY 535

RESULT 9
BID06308
ID BAD06308 PRELIMINARY; PRT; 638 AA.
AC BAD06308;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DE Vesicular GABA transporter.
GN Ciona intestinalis.
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RA SEQUENCE FROM N.A.
RP Yoshida R., Sakurai S., Horie T., Kawakami I., Tsuda M., Kusakabe T.;
RT "Identification of neuron-specific promoters in Ciona intestinalis.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB158401; BAD06308.1; -.
SQ SEQUENCE 638 AA; 69532 MW; 707CD701FB409FDA CRC64;

Query Match 46.7%; Score 1283.5; DB 2; Length 638;
Best Local Similarity 44.2%; Pred. No. 1.5e-86;
Matches 244; Conservative 88; Mismatches 117; Indels 103; Gaps 6;

QY 37 TDEAVGFAHCDLDFEHRQGLQMDILKAEGPCGDEGAAPVEGDI-HYQSGGAPLPP 95
Db 18 TSEKFSFAKSDQ-----HPSGSGCGGATNPSSNSVSHPERST----- 59
QY 96 SGSKDOVCGGEGFGHDKPKITANEAGNVTNAIQGMFVLGPLYAILHGGYLGFLIIFA 155
Db 60 -----SGVERPTITADAGNNVSNAIQGMFVLGPLYAILHGGYLGFLIILVIT 106
QY 156 AVVCCYTGKILIACTYBENEDGEVVRVDSYVAIANACCAPRFTLGGRVVNAQIIEVL 215
Db 107 AVVCCYTGKILIDCLYETSPSGERLVRSTVYDLAAHGWKH---LGLYLVAQAQLIELL 163
QY 216 MTCILYVVVSGNLMYNSPGLPVQSKWSIIATAVLLPCAFPLKLVKAVSFSLCTLAHF 275
Db 164 MTCVLYVVVSGNLMYNSPFGHPPIBEAGMSVLACILVLPFCFLRHLRAVSFSGCSVAQI 223
QY 276 VINIIVLAYCLSRDARDAWEKVKYIDVKFPPIIGIIVFSYTSOIFLPSLEGNMQOPSE 335
Db 224 VVLGITIVYCIKINTWAWSEITISVDMKQFVPSIGVIVFVSQIPLPSLESGMENRGD 283
QY 336 FHCMMNTHIAACVLKGLPALVAVLTWADETKEVITDNLPGSIRAVVNIPLVAKALLSYP 395
Db 284 FRSLMSVSYASCVTKASFALICFLTWSKOTDVTDLNPTLRAMINVLVLLVALLSYP 343
QY 396 LPFFAAVEVLEKSLF----- 410

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Db 344 LPYQAIEVMEQTMFTGATGGWSLFGTKRHAYGFTDDTEPIVQSTSFNTDAPSSPST 403
QY 411 -----QEG-----SRAFFPACVSGDGLKSWGLTRCALVFTLLMA 447
Db 404 TNSDGLDSDKSTTKRNVILTLEDNTKQSSCSPSCYSATGDLQVWALVLRAGLVLTLLMG 463
QY 448 IYVPHFALLMGLTSLTGAGLCFLPLSLFHLRLKLLMHQVFFDVAIFVIGGICSVSG 507
Db 464 VIPHPHALLMGLTSLTGSLAFPLPCAFHLQIKWREMKWREIGLDVFIISGTVCGITG 523
QY 508 FVHSLGLEIAY 519
Db 524 IYFSIQGLYEVY 535

RESULT 10
Q7QHB6
ID Q7QHB6 PRELIMINARY; PRT; 549 AA.
AC Q7QHB6;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE Ehip8381 (Fragment).
GN Name=ebig8381; ORFNames=ENSANGG00000006321;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RA SEQUENCE FROM N.A.
RP STRAIN=PEST;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05252.1; -.
DR GO; GO:0016270; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa trans; 1.
DR NON TER 549
FT SEQUENCE 549 AA; 60847 MW; 21A09BD0190E02A0 CRC64;

Query Match 39.3%; Score 1081.5; DB 2; Length 549;
Best Local Similarity 47.1%; Pred. No. 1.2e-71;
Matches 221; Conservative 80; Mismatches 141; Indels 27; Gaps 10;

QY 72 DEGAAP-----VEGDH--YQSGGAPLPPSGSKDQVGGGEGFG--HDKP-- 114
Db 81 EESTQPGTNQYQETGFGNGGFENGYQAG-GYP-PRQSGVQSFSDSTFAGCGEAPGG 138
QY 115 -KITAWAGNVTNAIQGMFVLGPLYAILHGGYLGFLIIFAAVCCYTGKILIACTY- 172
Db 139 AKINEYQAANVTNAIQGMFIVSLPFAVLGGYVALLAMVGIACICCTYTGKILVCLYEP 198
QY 173 ENEDGEVVRVDSYVAIANACCAPRFTLGGRVVNAQIIELVMTCTILYVVVSGNLMYNS 232
Db 199 DPQTGEVVRVDSYVSIKAVCFGRK---IGARVVSIAQIIELEMTCTILYVVVCGDLMAGS 255
QY 233 FPLGVSOKSIIATAVLLPCAFPLKLVKAVSFSLCTLAHFVINIIVLAYCLSRARDW 292
Db 256 PDGALDTRSMMLCGIIFLLPLAFKLSLHVHLSLSFWCTMAHLLINAIIVGCLLEIGDW 315
QY 293 AWEKVKFIDVKKPIISIGIIVFSYTSOIFLPSLEGNMQOPSEPHCMNTHIAACVLK 352
Db 316 GMSKVKWRMDPFENFISLGVIVFSYTSOIFLPLEGNMEDSKFNWMLDMSHIAAFAKA 375
QY 353 LFALVAVLTWADETKEVITDNL--PGSIRAVVNIPLVAKALLSYPPLPFFAAVEVLEKSLF 410
Db 376 LFGYICFLTQNDTQQVITNNLHSPG-FKGLVNECLVTKAILSYPLPFFAACELLERAPF 434

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Db 434 FRGPCKTPTTWNLDGELKWLGRVGVIVSTILMAIFPHPSILMGRIGSFTGTMLS 493

QY 470 FLPLSLFHLRLWLKHLWHQVFPDVAIVFVIGICSVSGFVHSLGLEIAY 519

Db 494 FIWPCYFIKIKHLLDQKEAKDYLIIGLVGVIGYDSGNALINAF 543

RESULT 12

UN47 CAEEL

ID UN47 CAEEL STANDARD; PRT; 486 AA.

AC P34579; O17475; DB 486 AA.

DT 01-FEB-1994 (Rel. 28, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Vesicular GABA transporter (Uncoordinated protein 47) (Protein unc-47).

GN Name=unc-47; ORFNames=T20G5.6;

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

XP [1] SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF GLY-462. MEDLINE=98007977; PubMed=9349821;

RA McIntire S.L., Reimer R.J., Schuske K., Edwards R.H., Jorgensen E.M.;

RT "Identification and characterization of the vesicular GABA transporter."

RL Nature 389:870-876 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Berks M., Smith A.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

RN [3]

RP REVISIONS.

RA Durbin R.;

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

CC -! FUNCTION: Involved in the uptake of GABA into the synaptic vesicles.

CC -! SUBCELLULAR LOCATION: Integral membrane protein. Intracellular membrane vesicles.

CC -! SIMILARITY: Belongs to the amino acid/polyamine transporter family II.

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DR EMBL; AF031935; AAB87066.1; -

DR EMBL; Z30423; CAAB3006.2; -

DR PIR; S42372; S42372.

DR PIR; T42254; T42254.

DR WormPep; T20G5.6; CE251119.

DR InterPro; IPR002422; AA/rel\_permease2.

DR Pfam; PF01490; AA\_trans; 1.

KW Glycoprotein; Neurotransmitter transport; Transmembrane; Transport.

FT DOMAIN 1 93 Cytoplasmic (Potential).

FT DOMAIN 94 114 Potential.

FT DOMAIN 115 119 Vesicular lumen (Potential).

FT DOMAIN 120 140 Potential.

FT DOMAIN 141 167 Cytoplasmic (Potential).

FT DOMAIN 168 188 Potential.

FT DOMAIN 189 203 Vesicular lumen (Potential).

FT DOMAIN 204 224 Potential.

FT DOMAIN 225 228 Cytoplasmic (Potential).

FT DOMAIN 229 249 Potential.

FT DOMAIN 250 263 Vesicular lumen (Potential).

FT DOMAIN 264 284 Potential.

FT DOMAIN 285 305 Cytoplasmic (Potential).

FT TRANSMEM 306 326 Potential.

FT DOMAIN 327 341 Vesicular lumen (Potential).

FT TRANSMEM 342 362 Potential.

FT DOMAIN 363 398 Cytoplasmic (Potential).

FT TRANSMEM 399 419 Potential.

FT DOMAIN 420 421 Vesicular lumen (Potential).

FT TRANSMEM 422 442 Potential.

FT DOMAIN 443 457 Cytoplasmic (Potential).

FT TRANSMEM 458 478 Potential.

FT DOMAIN 479 486 Vesicular lumen (Potential).

FT CARBOHYD 337 337 N-linked (GlcNAc...), (Potential).

FT MUTAGEN 462 462 G->R: In N2409; loss of GABA transport into synaptic vesicles.

SQ SEQUENCE 486 AA; 54439 MW; 6435C3B38552925 CRC64;

Query Match 31.2%; Score 858; DB 1; Length 486;

Best Local Similarity 40.4%; Pred. No. 3.7e-55;

Matches 180; Conservative 96; Mismatches 141; Indels 28; Gaps 8;

QY 75 AEAPVEGDHYQSGSGAPLPPSGSKDQVGGGEGFGHDKPKITAWAGNVTNAIQGMFV 134

Db 63 SQPQKDDINKQ-----BEAKDD--GHGE-----ASEPISALQAANVTNAIQGMFI 107

QY 135 LGIPYAILHGGYLGFLIIFPAWVCYTGKILLIACLYEENEDGEVVRDVSVAIANACC 194

Db 108 VGLPIAVKVGWWSIGAMVGVAVCYVGTGVLLECLYENG-----VKRKYTREIAD-FY 161

QY 195 APRFPTLGGRVNVAQIIELVMTCLIVVYVSGNLMYNSFPGLFVPSQKSMIIATAVLLPC 254

Db 162 KPGF---GKWLAAQTLSTLCIILVLAADLLQSCFES--VDKAGMMITSASLLTC 215

QY 255 AFLKNLKVSKFSLCTLAHFVNILVATYCLSRADWAKWKFYIDVKFPPIGIIIV 314

Db 216 SFLLDLQIVSRLSFFNAISHLIVNLMVLYCLSFVSQMSFSTITSLMINTLFTVGMV 275

QY 315 FSVTSOIFLPSLEGNNQOOPSEFHCMMNTHIAACVLKGLFALVAVLTWADETKEVITDNL 374

Db 276 FGYTSHIFLPNLEGNMKPAQFNWMLKWSHIAAAVFKVFGMLGELTQGEISNSL 335

QY 375 PG-STRAVNIFLVAKALLSYPLPFAAIVELEKSLFOEGSRAPFPACYSGGGRUKSWGL 433

Db 336 PQQSFKILNVLVVKALLSYPLPFAAIVQLKNNLFLGYPQTPFTSCYSPDKSREWAV 395

QY 434 TLRCALVWTLMAVYVPHFALLMGITGLTSCAGICELLPFLHLRLWLKHLWHQVFPD 493

Db 396 TLRIILVFLFVALSVPLVLMGLVGNITMLSFIPALFHLHYIKEKTLNLFKRPD 455

QY 494 VAIFVIGICSVSGFVHSLGLEIEA 518

Db 456 QGIIMGCSVCISGVVFSMELLRA 480

RESULT 13

Q8SPUO PRELIMINARY; PRT; 164 AA.

AC Q8SPUO;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Solute carrier family 32 member 1 (Fragment).

GN Name=SLC32A1;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Norgren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF489843; AAL96689.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

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DR GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa_trans; 1.
FT NON_TER 164 164
SQ SEQUENCE 164 AA; 18476 MW; F1131374A3810A65 CRC64;

Query Match 31.0%; Score 853; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 2.5e-55;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 VQIITELVNTCILYVVVSGNLMYNSFPGLPVSKWSIIATAVLLPCAFKLNKLVKAVSKFS 267
DB 1 VQIITELVNTCILYVVVSGNLMYNSFPGLPVSKWSIIATAVLLPCAFKLNKLVKAVSKFS 60
QY 268 LLCTLAHFVNTILYAYCLSRARDWAEKVKFYIDVKKFPIISIGIIVFSYTSQIFLPSLE 327
DB 61 LLCTLAHFVNTILYAYCLSRARDWAEKVKFYIDVKKFPIISIGIIVFSYTSQIFLPSLE 120
QY 328 GNNQPSSEPHCMNWNTHIAACVLKGLFALVAYLTWADTKVEIT 371
DB 121 GNNQPSSEPHCMNWNTHIAACVLKGLFALVAYLTWADTKVEIT 164

RESULT 14
QYXUV8 PRELIMINARY; PRT; 455 AA.
AC QYXUV8
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-NAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSUNBa0072F16.7 protein.
GN Name=OSUNBa0072F16.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL60460; CAD4982.2; --
DR Genbank; QYXUV8; --
DR GO:0016020; C:membrane; IEA.
DR GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa_trans; 1.
SQ SEQUENCE 455 AA; 47994 MW; 2F7CFE8B85CEDB00 CRC64;

Query Match 13.7%; Score 375.5; DB 2; Length 455;
Best Local Similarity 26.0%; Pred. No. 1.9e-19;
Matches 126; Conservative 84; Mismatches 200; Indels 75; Gaps 16;

QY 48 DDLDFHRQGLQMDILKABGE-PCGDEGAEEVGEIDHYQRSGAPLPSPSKQVGGGG 106
DB 21 EDSSTARRPDFQPLLOQAHPA--RGQEQEVEDRDEAQAQ-----CSPEDAGDA 68
QY 107 EFGGDKPKITAEWAGNWNVTAIQGMFVLGFLPYAILHGGYLGFLFIIFAAVCCYTKIL 166
DB 69 TF-----VRTCENGLNALSGVLLSIPYALSEGGLSLVLLLAAMVCCYTGILL 118

167 IACLYBENEDGEVVRVDSYVAIANACCAPRFTLGGRVVNVVAQIIELVNTCILYVVVSG 226
119 RRCW----AASPAVRGYPDICALA-----FGAKGLAVSAFLYAELVLAICFLILEG 167
227 NLYNSFP-----GLPVSKWSIIATA-VLLPCAFKLNKLVKAVSKFSLLCTLAHFVN 278
168 DNCKLFPPTGSLAVGGLVSGKQLFVVVAVVILPTTWLRSVLAVLVUS-----ASGVLA 222
279 ILVIAYCLSRARDWA--WEKVKFY-----IDVKKFPIISIGIIVFSYTSQIFLPSLEGNMQ 331
223 SVVVFVCL----WAAVFDGCVGFHGRMLNVSGLPTALGLYFCYCGHAIFPTLCNSMQ 278
332 QPSEFHCMMWNTHIAACVLKGLFALVAYLTWADTKVEITDNLV-PSIRAVNVIF-LVAK 389
279 EKDKFSVLVVICVACTVNYGSMAILGYLMYGDVKSQVTLNLPFGKISKLAITYTLIN 338
390 ALLSYPLPFPFAAEEVLEKSLFOEGSRAFFPACYSYGGRLKSMGLTLRLCALVWFTLLMAIY 449
339 PFSKYALMVTVPVATAIEKLLA-----GNKESVNVLIRTLIVVSTVIALT 384
450 VPHFALLMGLTSGITGAGLCFLPSPFLHLLWRKLLWH-QVFFDVAFIVGIGICSVSGF 508
385 VPFFGHLMALVGSLLSYMASMLLPCICYLKIFGLTRCGRGETLLIAAIIVLGSLVAATGT 444
509 VHSLE 513
445 YSSLK 449

RESULT 15
QYU97 PRELIMINARY; PRT; 571 AA.
AC QYU97
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative amino acid transport protein.
GN Name=B1370C05.10-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005873; BAB08181.1; --
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa_trans; 1.
SQ SEQUENCE 571 AA; 62625 MW; 30312268725FB4DA CRC64;

Query Match 13.4%; Score 367.5; DB 2; Length 571;
Best Local Similarity 26.7%; Pred. No. 9.6e-19;
Matches 116; Conservative 93; Mismatches 175; Indels 61; Gaps 11;

QY 113 KPKITAE-----AGWNVTNAIQGMFVLGFLPYAILHGGYLGFLFIIFAAVCCY 161
DB 169 KPLVPAHEVPAYQOCSTQAVNMGINVLGCVGILSTPYAIKQGGWLGVLICLFAVLAWY 228
162 TGKILIACTLYEENEDGEVVRVDSYVAIANACCAPRFTLGGRVVNVVAQIIELVNTCILY 221
229 TGVLLRRLCL--DSKEG-----LETYPDIGHAA-----FGTGTGRTAISILYIELYACCI 277
222 VVYSGNLMYNSFPGLPV-----SQKWSIIATAVLLPCAFKLNKLVKAVSKFSLLCTLA 273
278 LILESNDLSKLFNNAHLTIGSMTLNSHVFPAILTTLIVMPTTWLRLDLSCLSYLS-----A 332
274 HFVINILVIAYCLSRARDW-----AWKVKFYIDVKKFPIISIGIIVFSYTSQIFLPSL 326
333 GGVIASILVVVCLC----WYGVVDVHGVFNKGTALNLP-GPIAIGLYGVCYSGHGVFPNI 388
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QY 327 EGNMQPSEPHCMNWTHTIACVLKGLFALVAYLTWADETKEVITDNLPGS--IRAVVNI 384
Db 389 YSSLKRNQFPSSILFTCTIGLSILFAGAAVGYKMGESTESQFTNLDPENLVVSKVAVW 448
QY 385 FLVAKALLSYPLPFFFAAVEVELEKSLFQEGSRAFFPACYSYGDRLKSWGLTLRCALVVFTL 444
Db 449 TTVANPITKYALTITPLAMSLLEELLPPNQK-----YANI-----IMLRSSLVVSTL 495
QY 445 LMAIYVPHFALLMGLTGSITGAGLCFLLPSLFHLRLWRKLLWHQVDFDVAIFVIGICS 504
Db 496 LIALSVPPFGLVMAVGSLLTMLVTYILPCACFLAILKRVKVTWHQIAACSFIIVGVCCA 555
QY 505 VSGFVHSLEGLIEAY 519
Db 556 CVGTYSLSLKIIQNY 570

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Search completed: November 8, 2004, 18:55:05  
Job time : 473 secs